

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 19:27:38 ; Search time 5980 Seconds

(without alignments)
9757.708 Million cell updates/sec

Title: US-09-967-305-1

Perfect score: 2005 1 ttgcagcgcctgctggctggg.....acatccagaataaattct 2005

Sequence: 1 ttgcagcgcctgctggctggg.....acatccagaataaattct 2005

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pt:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hg_hum:*

31: em_hg_in:*

32: em_hg_om:*

33: em_hg_ov:*

34: em_hg_pat:*

35: em_hg_ph:*

36: em_hg_pl:*

37: em_hg_pt:*

38: em_hg_ro:*

39: em_hg_sts:*

40: em_hg_un:*

41: em_hg_vl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2005	100.0	2005	9	AF158378
2	1993.8	99.4	2041	9	AF047020
3	1950.8	97.3	2068	9	AF130723
4	1653.2	82.5	1674	9	AK000912
5	1616.8	80.6	2946	9	BC009471
6	1574.2	78.5	1621	6	AX106326
7	1574.2	78.5	1621	6	AX140617
8	1574.2	78.5	1621	6	AX200477
9	1574.2	78.5	1621	6	AX267133
10	1201.4	59.9	131856	9	AC008954
11	1201.4	59.9	131856	9	AC008971
12	1201.4	59.9	155013	2	AC026707
13	830	41.4	1504	6	AX401900
14	830	41.4	1504	6	RN089905
15	807	40.2	1498	10	RN2491CO
16	804	40.1	1317	9	AK022765
17	792.6	39.5	1472	10	BC015825
18	785.8	39.2	1515	10	MM089906
19	515	25.7	537	6	AX106293
20	515	25.7	537	6	AX140584
21	515	25.7	537	6	AX200444
22	515	25.7	537	6	AX267100
23	428.4	21.4	430	6	AX368794
24	406.6	20.3	773	6	AX106222
25	406.6	20.3	773	6	AX140513
26	406.6	20.3	773	6	AX200373
27	406.6	20.3	773	6	AX267029
28	403.2	20.1	793	6	AX106252
29	403.2	20.1	793	6	AX140543
30	403.2	20.1	793	6	AX200403
31	403.2	20.1	793	6	AX267059
32	400.2	20.0	816	6	AX140512
33	400.2	20.0	816	6	AX200372
34	400.2	20.0	816	6	AX267028
35	365	18.2	412	11	G21632
36	347.4	17.3	421	6	AX302796
37	330.4	16.5	354	6	AX336296
38	321	16.0	140132	2	AC128089
39	290	14.5	301	6	AX106461
40	290	14.5	301	6	AX140752
41	290	14.5	301	6	AX200612
42	290	14.5	301	6	AX267268
43	289	14.4	301	6	AX106471
44	289	14.4	301	6	AX140762
45	289	14.4	301	6	AX140762

ALIGNMENTS

RESULT 1

AF158378

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 2005)

Ferdinandusse,S., Denis,S., Clayton,P.T., Graham,A., Rees,J.E., Allen,J.T., McLean,B.N., Brown,A.Y., Vreken,P., Waterham,H.R. and Wanders,R.J.

2005 bp mRNA linear PRI 11-FEB-2000

AF158378

AF158378.1 GI:6653127

2005 bp mRNA linear complete cds

5/9/03

TITLE Mutations in the gene encoding peroxisomal alpha-methylacyl-CoA racemase cause adult-onset sensory motor neuropathy

JOURNAL Nat. Genet. 24 (2), 188-191 (2000)

MEDLINE 20120722

PUBMED 10635068

REFERENCE 2 (bases 1 to 2005)

AUTHORS Ferdinandusse, S., Denis, S. and Wanders, R.J.A.

TITLE Direct Submission

JOURNAL Submitted (11-JUN-1999) Clinical Chemistry, Academic Medical Center, Meibergdreef 9, Amsterdam 1105 AZ, the Netherlands

FEATURES

source

1. .2005

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="skin fibroblast"

1. .2005

/gene="RM"

66. .1214

/gene="RM"

/function="racemisation of stereoisomers of 2-methyl-branched chain fatty acyl-CoA esters"

/product="alpha-methylacyl-CoA racemase"

/codon_start=1

/protein_id="AAF22610.1"

/db_xref="GI:6653128"

/translation="MALQGISVVELSGLAAPFPCAMVLADFGARVVRDPSRVDYSRLGRKSLVLDLKOPRGAIVRLCKRSDVLEPPRRGMELQSGPELQENRRLIYARLSGPGSGSFCRLAGHDINYLALSVLSTIGSGACNPYPLIPLADPGENGLALGIMALDRLRTGKGYIDANMEGTAYLSFLFKTKSSIMEPRONMIDGAPFTTTRTAGDEPMAVGAIPEQFELIKIGLSDLPQMSMDHPEPKKKFADVFAKTKAEWCQIFDGTADACVTPVLFEEVHHDHNRKESF ITSEQDVSPPAPLLINTPAIPSEKRPDIETHEETLEEFGRREIYQINSDKIIESNKKASL"

90

/gene="RM"

/replace="a"

589

/gene="RM"

/replace="a"

667

/gene="RM"

/replace="t"

783

/gene="RM"

/replace="t"

894

/gene="RM"

/replace="g"

BASE COUNT 519 a 427 c 514 g 545 t

ORIGIN

Query Match 100.0%; Score 2005; DB 9; Length 2005;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 CTTCCGCGCGGTCATGAGAAACTCCAGTGGGCCAGAGATTCTCACGGGAAA 360

DB 301 CTTCCGCGCGGTCATGAGAAACTCCAGTGGGCCAGAGATTCTCACGGGAAA 360

QY 361 ATCCAAAGCTTATTTATGACAGGCTGATGATTTGGCCAGTGAAGCTTCCGGT 420

DB 361 ATCCAAAGCTTATTTATGACAGGCTGATGATTTGGCCAGTGAAGCTTCCGGT 420

QY 421 TAGTGGCCACGATATCACTATTTGGCTTGTACAGTGTCTCTCAAAATTTGGCAGAA 480

DB 421 TAGTGGCCACGATATCACTATTTGGCTTGTACAGTGTCTCTCAAAATTTGGCAGAA 480

QY 481 GTGATGAAATCCGATAGCCCGCTGATCTCCGTGGCTGATGCTGTGGTGGCCTTA 540

DB 481 GTGATGAAATCCGATAGCCCGCTGATCTCCGTGGCTGATGCTGTGGTGGCCTTA 540

QY 541 TGTGTGACCTGGGCAATTAATGAGCTCTTTTGAACGACACGACACTGGCAAGGTCAGG 600

DB 541 TGTGTGACCTGGGCAATTAATGAGCTCTTTTGAACGACACGACACTGGCAAGGTCAGG 600

QY 601 TCAATGATGCAATTAATGAGCTCTTTTGAACGACACGACACTGGCAAGGTCAGG 660

DB 601 TCAATGATGCAATTAATGAGCTCTTTTGAACGACACGACACTGGCAAGGTCAGG 660

QY 661 AGAAATGACCTGTGGGGAAGCACTTCGAGACAGAACATGTTGATGTGGAGACACTT 720

DB 661 AGAAATGACCTGTGGGGAAGCACTTCGAGACAGAACATGTTGATGTGGAGACACTT 720

QY 721 TCTATACGACTTACAGACAGCAGATGGGAATTCATGCTGTGGAGCAATAGAACCC 780

DB 721 TCTATACGACTTACAGACAGCAGATGGGAATTCATGCTGTGGAGCAATAGAACCC 780

QY 781 AGTTCTACGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

DB 781 AGTTCTACGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

QY 841 TGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

DB 841 TGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

QY 901 CGAAGGCAAGAGTGTGCAAAATCTTTGACGCGACAGATGCTGTGACCTCCGCTTGA 960

DB 901 CGAAGGCAAGAGTGTGCAAAATCTTTGACGCGACAGATGCTGTGACCTCCGCTTGA 960

QY 961 CTTTGAAGAGGTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

DB 961 CTTTGAAGAGGTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1021 AGGAGCAGAGCTGAGGCGCCGCTGACCTGCTGTTAAACACCCAGCATCCCTT 1080

DB 1021 AGGAGCAGAGCTGAGGCGCCGCTGACCTGCTGTTAAACACCCAGCATCCCTT 1080

QY 1081 CTTTCAAAAGGATCCTTTATAGGAGAACACACTGAGGAGATCACTTGAAGATTGGAT 1140

DB 1081 CTTTCAAAAGGATCCTTTATAGGAGAACACACTGAGGAGATCACTTGAAGATTGGAT 1140

QY 1141 TCAAGCCGGAAGATTATACAGCTTAACACATTAATTAATTAATTAATTAATTAATTAAT 1200

DB 1141 TCAAGCCGGAAGATTATACAGCTTAACACATTAATTAATTAATTAATTAATTAATTAAT 1200

QY 1201 AAGCTAGCTCTAATCTTCAAGGCGCCAGGCTCAAGTGAATTTGAATTAATTAATTAAT 1260

DB 1201 AAGCTAGCTCTAATCTTCAAGGCGCCAGGCTCAAGTGAATTTGAATTAATTAATTAAT 1260

QY 1261 GTAGAGTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320

DB 1261 GTAGAGTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320

QY 1321 ACCACTTAATCAAGAAAGAAATTAACAGACTGTGATTTACAGTGTGATGATGATGATGAT 1380

DB 1321 ACCACTTAATCAAGAAAGAAATTAACAGACTGTGATTTACAGTGTGATGATGATGATGAT 1380

Qy	1381	AAATGGTATCATTAAGGCGCTTTGATTATTAACCTTGGTACTATACATAATATG	1440
Db	1381	AAATGGTATCATTAAGGCGCTTTGATTATTAACCTTGGTACTATACATAATATG	1440
Qy	1441	TATTTATTCGCTTCAGTTTCCTTGATATATTTGGTATATTAAGATCTGACATT	1500
Db	1441	TATTTATTCGCTTCAGTTTCCTTGATATATTTGGTATATTAAGATCTGACATT	1500
Qy	1501	AATTTGAATGGGTTCTGATGAAAAGGATATATATTTCTTGAACATCGATATACAT	1560
Db	1501	ATTTTGAATGGGTTCTGATGAAAAGGATATATATTTCTTGAACATCGATATACAT	1560
Qy	1561	TATTTTACACTCTTATTTCTACAAATGTAGAAAATGAGAAATGCCACAAATGTATGTGA	1620
Db	1561	TATTTTACACTCTTATTTCTACAAATGTAGAAAATGAGAAATGCCACAAATGTATGTGA	1620
Qy	1621	TAAAAATCAGTGAACAGAGTATGGTTCATCCAGGCGCTTTGTCCTGTGATG	1680
Db	1621	TAAAAATCAGTGAACAGAGTATGGTTCATCCAGGCGCTTTGTCCTGTGATG	1680
Qy	1681	ATCTCCCTCTAAGCACATTTCCAAACTTTAGCACAGTATACACACTTTGTATATGGCAA	1740
Db	1681	ATCTCCCTCTAAGCACATTTCCAAACTTTAGCACAGTATACACACTTTGTATATGGCAA	1740
Qy	1741	GAAAGTTTCACTCGTATTTGAATCAAGTAATGCCCTTCACTGAAAAAACAATCCAAATA	1800
Db	1741	GAAAGTTTCACTCGTATTTGAATCAAGTAATGCCCTTCACTGAAAAAACAATCCAAATA	1800
Qy	1801	ATGAGGAATATGTGTGGCTCAGTACAGTAGAGTCAGAGGAGCAGTACAGTTTAGAGTTGC	1860
Db	1801	ATGAGGAATATGTGTGGCTCAGTACAGTAGAGTCAGAGGAGCAGTACAGTTTAGAGTTGC	1860
Qy	1861	CTGTATCCAGTAATCGGGGCGTGTTCGCCGTGGGCTGTGGGCGTACAGTTTCCCTT	1920
Db	1861	CTGTATCCAGTAATCGGGGCGTGTTCGCCGTGGGCTGTGGGCGTACAGTTTCCCTT	1920
Qy	1921	CTCATAGTGTATTTCTTCCTCAGGCGTAGCAAGTCTTGATCTTATACCCACACA	1980
Db	1921	CTCATAGTGTATTTCTTCCTCAGGCGTAGCAAGTCTTGATCTTATACCCACACA	1980
Qy	1981	CAGCAACATCCAGAAATTAAGTTCT	2005
Db	1981	CAGCAACATCCAGAAATTAAGTTCT	2005
RESULT 2			
LOCUS	AF047020	2041 bp	mRNA linear PRI 29-JAN-1999
DEFINITION	Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.		
ACCESSION	AF047020		
VERSION	AF047020.1	GI:4204096	
KEYWORDS			
ORGANISM	Homo sapiens.		
SOURCE	Homo sapiens.		
REFERENCE			
TITLE	1 (bases 1 to 2041)		Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
AUTHORS	Albers, C., Schmitz, W. and Conzelmann, E.		
JOURNAL	Human alpha-methylacyl-CoA racemase cDNA sequence		
REFERENCE			
TITLE	2 (bases 1 to 2041)		
AUTHORS	Albers, C., Schmitz, W. and Conzelmann, E.		
JOURNAL	Direct Submission		
TITLE	Submitted (06-FEB-1998) Blozentrum, University of Wuerzburg, Am		
REFERENCE			
TITLE	3 (bases 1 to 2041)		
AUTHORS	Albers, C., Schmitz, W. and Conzelmann, E.		
JOURNAL	Submitted Submission		
TITLE	Submitted (29-JAN-1999) Blozentrum, University of Wuerzburg, Am		
REMARK	Hubland, Wuerzburg D-97074, Germany		
COMMENT	Sequence update by submitter		
FEATURES	On Jan 29, 1999 this sequence version replaced gi:2896147.		
	Location/Qualifiers		

	source	1..2041
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
CDS	89..1237	
	/EC_number="5.1.99.4"	
	/function="racemization of 2-methyl-branched fatty acid CoA esters"	
	/note="required for bile acid synthesis and for catabolism of branched-chain fatty acids"	
	/product="alpha-methylacyl-CoA racemase"	
	/codon_start=1	
	/protein_id="AAD1025.1"	
	/db_xref="GI:4204097"	
	/translation="MADGGISVMEISGLAPGFCAMVLADFGARYVRDPSGRDYVSRLGRKSLVDLKLQPRAAVLRRLLCRSDYLDLEFRFVGWEKLGIPITLORENPRLIVRSLRFSGSQCFLRHGDINYLALSVLSLRIRSESNPYAPMLLADPAGGLACALQIIMALFDRTDRDKSQVIDADMVEGTAYLSFFLMKTOKRSILMEAPRONNLDGARFYTTYATADGEPMAVGAIEPOPEELIKQLGISPELSOMSDIDMEPKKKKFADVPAKRKAAMCOIDEGTDCVTPLVFEEVVNHINDHKRSFIITSEODVSPRAPAFLLNTWPAISFKRPDPFGEHTETILEEFGFREBITOLNSDXIIESNKVKASL"	
BASE COUNT	525 a 441 c 527 g 548 t	
ORIGIN		
Query Match	99.4%; Score 1993.8; DB 9; Length 2041;	
Best local Similarity	99.7%; Pred. No. 0;	
Matches 1998:	Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Oy	1 TTGCAGCGCTGTGGCGTCGGGGCCTCAAGGCTCCCTCAGTTTCTCTTGACAGCGGGACTGTGGAA 60	
Db	24 TTGCAGCGCTGTGGCGTCGGGGCCTCAAGGCTCCCTCAGTTTCTCTTGACAGCGGGACTGTGGAA 83	
Oy	61 GGCCCATGGCACTCAGAGCATCTGGTCTGAGAGCTGTCCGCCCTGGCCCCGGCCCGCT 120	
Db	84 GGCCCATGGCACTCAGAGCATCTGGTCTGAGAGCTGTCCGCCCTGGCCCCGGCCCGCT 143	
Oy	121 TCGTGCTATGCTGCTGGTGAGATTGCGGGCGGTGTGTGTAAGCTGTGACCGCCCGCCGCT 180	
Db	144 TCGTGCTATGCTGCTGGTGAGATTGCGGGCGGTGTGTGTAAGCTGTGACCGCCCGCCGCT 203	
Oy	181 CCGCGTACGACGTAGCCGCTTGGCGCGGGCACAGCCCTGCTAGTGTGACACTGAAC 240	
Db	204 CCGCGTACGACGTAGCCGCTTGGCGCGGGCACAGCCCTGCTAGTGTGACACTGAAC 263	
Oy	241 AGCGCGGGAGCGCGCTGTCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 300	
Db	264 AGCGCGGGAGCGCGCGCTGTCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 323	
Oy	301 CCTTCCGCGCGGTGTCTATGGAGAAACTCAGCTGTGGGCCAGAGATCTGTGACGGGGAAA 360	
Db	324 CCTTCCGCGCGGTGTCTATGGAGAAACTCAGCTGTGGGCCAGAGATCTGTGACGGGGAAA 383	
Oy	361 ATCCAAGGCTATTATATGACGAGCTGACTGGATTGTGGCCAGTAGAGAGCTTGTGCCGT 420	
Db	384 ATCCAAGGCTATTATATGACGAGCTGACTGGATTGTGGCCAGTAGAGAGCTTGTGCCGT 443	
Oy	421 TAGCTGGCGACGATATCAACTATTGGCTTGTGTAGTGTCTCTCAAAAAATTGGCAGA 480	
Db	444 TAGCTGGCGACGATATCAACTATTGGCTTGTGTAGTGTCTCTCAAAAAATTGGCAGA 503	
Oy	481 GTGTGGAGAATTCGTATGCCCGCGTGATATCTCGGTGTACTTGTGTGTGTGGTGGCTTA 540	
Db	504 GTGTGGAGAATTCGTATGCCCGCGTGATATCTCGGTGTACTTGTGTGTGTGGTGGCTTA 563	
Oy	541 TGCTGTGACCTGGGATATATAAGGCTTTTGTGACCGCACACGACCTGTACAAGGGTCAGG 600	
Db	564 TGCTGTGACCTGGGATATATAAGGCTTTTGTGACCGCACACGACCTGTACAAGGGTCAGG 623	
Oy	601 TCATTGATGCAATATGTGTGGAAGAACAGCATATTTAAAGTTCTTTTCTGTGAAAACTC 660	
Db	624 TCATTGATGCAATATGTGTGGAAGAACAGCATATTTAAAGTTCTTTTCTGTGAAAACTC 683	
Oy	661 AQAATTCAGTCTGTGGGAAGCACTTCGAGAGCAAGACATGTTGATGTGTGACCACCTT 720	

```

Db 684 AGAATCGAGCTGTGGGAAGCAGCTCGAGGACAGAACATGTTGGATGGTAGCACCTT 743
Oy 721 TCTATACGACTTACAGAGACGAGATGGGAATTCATGGCTGTGGAGCAATPAGACCCC 780
Db 744 TCTATACGACTTACAGAGACGAGATGGGAATTCATGGCTGTGGAGCAATPAGACCCC 803
Oy 781 ACTTACGAGCTGTGATCAAGACGCTTGAATAAAGTCTGTGAAGTCTCCCATCAGA 840
Db 804 AGTTACGAGCTGTGATCAAGACGCTTGAATAAAGTCTGTGAAGTCTCCCATCAGA 863
Oy 841 TGAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGGCAAGAA 900
Db 864 TGAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGGCAAGAA 923
Oy 901 CGAAGCAGATGATGATTTGAATCTTTGAGGCGACAGATGCTGTGACATCCGCTCTGA 960
Db 924 CGAAGCAGATGATGATTTGAATCTTTGAGGCGACAGATGCTGTGACATCCGCTCTGA 983
Oy 961 CTTTGGAGAGGTTGTTTCATGATGATCACAACAGAGAGGCGGCTGTTTATCACCAGTG 1020
Db 984 CTTTGGAGAGGTTGTTTCATGATGATCACAACAGAGAGGCGGCTGTTTATCACCAGTG 1043
Oy 1021 AGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db 1044 AGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1103
Oy 1081 CTTTCAAAAGGAGTCTTTCATGAGAACACACATGAGAGAGATGATGAAATTTGGAT 1140
Db 1104 CTTTCAAAAGGAGTCTTTCATGAGAACACACATGAGAGAGATGATGAAATTTGGAT 1163
Oy 1141 TCAGCCGCGAGAGATTTTACGCTTAACTCAGATGATGATGATGATGATGATGATGATGAT 1200
Db 1164 TCAGCCGCGAGAGATTTTACGCTTAACTCAGATGATGATGATGATGATGATGATGATGAT 1223
Oy 1201 AAGCTAGTCTTCACTTCCAGGCGCCAGGCTCAGTGAATTTGAATTTGATTTGATTTGATTTGAT 1260
Db 1224 AAGCTAGTCTTCACTTCCAGGCGCCAGGCTCAGTGAATTTGAATTTGATTTGATTTGATTTGAT 1283
Oy 1261 GTAGATTAACATTAACATTTGATGATGAGAAACATGAGAGAGATGATGATGATGATGATGATGAT 1320
Db 1284 GTAGATTAACATTAACATTTGATGATGAGAAACATGAGAGAGATGATGATGATGATGATGATGAT 1343
Oy 1321 ACCACCTATCAAGAAAGAAATTTACAGACTGATTTACAGATGATGATGATGATGATGATGATGAT 1380
Db 1344 ACCACCTATCAAGAAAGAAATTTACAGACTGATTTACAGATGATGATGATGATGATGATGATGAT 1403
Oy 1381 AATGCTATCATTTAGGCTTTGATTTTAAACTTTGGGTAATTTACTAATTTATG 1440
Db 1404 AATGCTATCATTTAGGCTTTGATTTTAAACTTTGGGTAATTTACTAATTTATG 1463
Oy 1441 TATGATATCTGCTTCAGTTGCTGATATATTTGATATTTGATATTTGATATTTGATATTTGATATTT 1500
Db 1464 TATGATATCTGCTTCAGTTGCTGATATATTTGATATTTGATATTTGATATTTGATATTTGATATTT 1523
Oy 1501 ATTTTGAAGGCTTGAAGAAAGAAAGATGATATTTCTTGAAGACATGATATTCATT 1560
Db 1524 ATTTTGAAGGCTTGAAGAAAGAAAGATGATATTTCTTGAAGACATGATATTCATT 1583
Oy 1561 TATTTACATCTTGATTTACAAATGAGAAATGAGAAATGAGCAAAATTTGATGTTGA 1620
Db 1584 TATTTACATCTTGATTTACAAATGAGAAATGAGAAATGAGCAAAATTTGATGTTGA 1643
Oy 1621 TAAAGTCACTGTAAGACAGATGATTTGATTCATCCAGGCTTTGCTTGGTGTTCAGT 1680
Db 1644 TAAAGTCACTGTAAGACAGATGATTTGATTCATCCAGGCTTTGCTTGGTGTTCAGT 1703
Oy 1681 ATCTCCCTTAAAGCAGATTTCAAACTTTAGCAACAGTTATCACACTTTGATTTGCAAA 1740
Db 1704 ATCTCCCTTAAAGCAGATTTCAAACTTTAGCAACAGTTATCACACTTTGATTTGCAAA 1763
Oy 1741 GAAAGATTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1764 GAAAGATTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1823

```

```

Oy 1801 ATGAGAAATGTTGGTCTCACTACGTAGAGTCCAGAGGAGAGTCAAGTTTGGGTTGC 1860
Db 1824 ATGAGAAATGTTGGTCTCACTACGTAGAGTCCAGAGGAGAGTCAAGTTTGGGTTGC 1883
Oy 1861 CTGTATCCAGTAACTCGGGGCTGTTTCCCGTGGTCTCTGGGCTGTAGCTTTCTTT 1920
Db 1884 CTGTATCCAGTAACTCGGGGCTGTTTCCCGTGGTCTCTGGGCTGTAGCTTTCTTT 1943
Oy 1921 CTCATGCTGTTGATTTCTCTCAGGCTGTTAGCAAGTCTGAGTCTTATACCAACACA 1980
Db 1944 CTCATGCTGTTGATTTCTCTCAGGCTGTTAGCAAGTCTGAGTCTTATACCAACACA 2003
Oy 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
Db 2004 CAGCAACATCCAGAAATTAAGTTCT 2028

RESULT 3
HSA130733
LOCUS HSA130733 Homo sapiens mRNA 2-methylacyl-CoA racemase. 2068 bp linear PRI 30-NOV-2001
DEFINITION A130733
ACCESSION A130733 GI:4995298
VERSION A130733.1
KEYWORDS 2-methylacyl-CoA racemase.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Amery, L., Fransen, M., De Nys, K., Mannaerts, G. P. and Van Veldhoven, P. P.
Mitochochdrial and peroxisomal targeting of 2-methylacyl-CoA racemase in human
J. Lipid Res. 41 (11), 1752-1759 (2000)
PUBMED 11060344
REFERENCE 2 (bases 1 to 2068)
AUTHORS Van Veldhoven, P. P.
Direct Submission
Submitted (22-JAN-1999) Van Veldhoven P. P., Campus Gasthuisberg, Afdeling Farmakologie, Katholieke Universiteit Leuven, Herestraat, B-3000 Leuven, BELGIUM
REMARK Revisited by Author
FEATURES
source Location/Qualifiers
1..2068
/organism="Homo sapiens"
/db_xref="taxon:9606"
89..1237
/codon_start=1
/product="2-methylacyl-CoA racemase"
/protein_id="CAB44062.1"
/db_xref="GI:4995298"
/db_xref="SWISS-PROT:O9UHK6"
/translation="MALOGISVLESLGASLAPGXCMVLADFGARVRYRDRGSRVDS NLGRKRLVLEDKQPREPRAASVQAVGCAAGALPRECHETPAGPDSAGKSKAY LCQAEIMWPVESEFCRLAGHDINVLALSGLVSKTGRSENPAPLNLVADPAGGLMC ALGIMALEDRTRDQGVIDANVEGTAYLSFLLMKQKSLMWPAGOMNLDGAF FYTTRTADGEPMAGVLEPOVELLIGLGLKSDLELNOMSTDMWPMKKKFDVFA KKTAKMCOIDGDTDCVTPVLTREEVVHHNKRGRSFTISEEDVSPRLAPLLNT PAIRSSKDPRTGENTETLEIFEGSRREIYQNSDKTIIESNKVYASL."
BASE COUNT 555 a 436 c 528 g 548 t 1 others
ORIGIN
Query Match 97.3%; Score 1950.8; DB 9; Length 2068;
Best Local Similarity 98.9%; Pred. No. 0; Mismatches 18; Indels 4; Gaps 2;
Matches 1985; Conservative 0;
Oy 1 TTGAGGCTGTGGGCTGAGGCTTAAGGCTGCTCAAGTTCTTCTTCAAGCGGGGCACTGGGAA 60
Db 24 TTGAGGCTGTGGGCTGAGGCTTAAGGCTGCTCAAGTTCTTCTTCAAGCGGGGCACTGGGAA 83
Oy 61 GCGCCATGCGACTGCAAGGCAATCTCGTGTGAGAGCTGTCCGGCCCTGCGGCCGCCGCT 120

```

D	b	84	GGCCGATGGCACTGCAGGGGCATCTTCGGTCTGTGAGCTGTCCGGCTTGGCCCCGGGCCGTN	143
O	y	121	TCATGCTATAGGTCTCTGGCTACATCTTGGGGCCGCTGTGGTACGCTGGACCGCCGGCT	180
D	b	144	TCATGCTATAGTCTCGGTACTCTCGGGCCGCTGTGGTACGCTGGACCGCCGGCCGT	203
O	y	181	CCGGCTACGACTGAGCCGCTTGGGGCCGGGGCAAGCGCTCGTAGTGGCTGGACCTGAAGC	240
D	b	204	CCGGCTACGACTGAGCCGCTTGGGGCCGGGGCAAGCGCTCGTAGTGGCTGGACCTGAAGC	263
O	y	241	AGCCGGGGGAAGCCGCTGTGCTGCGGCGCTGTGTCAGAGCGTGGAGTGTGCTGTGGAGC	300
D	b	264	AGCCGGGGG - AGCCGCGCTGTGCGGGCTGTGTGGCAAGGGCTGGAGTGTGCTGTGGAGC	321
O	y	301	CTTTCCGCCGCGGTGTCAATGGAGAAATCCAGTGGGGCCAGAGATTTCTGCAGCGGGAAA	360
D	b	322	CTTTCCGCCGCGGTGTCAATGGAGAAATCCAGTGGGGCCAGAGATTTCTGCAGCGGGAAA	381
O	y	361	ATCCAAAGGCTTTATTTATCCCAAGGCTGAGTGGATTTGGGCCAGT - CAGSAAAGCTTCTCGC	418
D	b	382	ATCCAAAGGCTTTATTTATCCCAAGGCTGAGTGGATTTGGGCCAGTTCAGSAAAGCTTCTCGC	441
O	y	419	GTTAGCTGCGCCAGATATCACTATTTAGGCTTTGTGCAGGGTGTCTCTCAAAAATTTGGAG	478
D	b	442	GTTAGCTGCGCCAGATATCACTATTTAGGCTTTGTGCAGGGTGTCTCTCAAAAATTTGGAG	501
O	y	479	AAGTGGAGGAATCCGTTATGCGCCGCGGTAAATCTCTGGCGTGAATTTGCTGGTGGGGGCT	538
D	b	502	AAGTGGAGGAATCCGTTATGCGCCGCGGTAAATCTCTGGCGTGAATTTGCTGGTGGGGGCT	561
O	y	539	TATGTGTGCACTGGGCAATTAATATATGAGCTTTTGTGACCCAGACAGCACTGGCAAGGTCA	598
D	b	562	TATGTGTGCACTGGGCAATTAATATATGAGCTTTTGTGACCCAGACAGCACTGGCAAGGTCA	621
O	y	599	GGTCATTTGATGCAATTAATATATGAGGAGAAAGCAAGATTTAACTCTTTTCTGTGAAAAC	658
D	b	622	GGTCATTTGATGCAATTAATATATGAGGAGAAAGCAAGATTTAACTCTTTTCTGTGAAAAC	681
O	y	659	TCGAAATTCGATCTGTGTGGGAAGCACTCCAGAGACAGAACTGTGTGATGGTGGAGCAC	718
D	b	682	TCGAAATTCGATCTGTGTGGGAAGCACTCCAGAGACAGAACTGTGTGATGGTGGAGCAC	741
O	y	719	TTTTCTATACGACTTACAGAGACAGAGATGGGGAATTCATGGCTGTGTGGAGCAATGAACC	778
D	b	742	TTTTCTATACGACTTACAGAGAGAGAGATGGGGAATTCATGGCTGTGTGGAGCAATGAACC	801
O	y	779	CCAGTTCTACGAGCTGCTGATCAAGAACTTTGAACTGTGATGAATCTTCCCAATCA	838
D	b	802	CCAGTTCTACGAGCTGCTGATCAAGAACTTTGAACTGTGATGAATCTTCCCAATCA	861
O	y	839	GATGAGCATGAGTGAATTTGGCCAGAAATGAAGAAGATTGGAGATGATTTGGCAAGAA	898
D	b	862	GATGAGCATGAGTGAATTTGGCCAGAAATGAAGAAGATTGGAGATGATTTGGCAAGAA	921
O	y	899	GAGGAGGAGAGATGTGTGCAAAATCTTTGACGGGACAGATGCTGTGTGACCTCGGGTTCT	958
D	b	922	GAGGAGGAGAGATGTGTGCAAAATCTTTGACGGGACAGATGCTGTGTGACCTCGGGTTCT	981
O	y	959	GACCTTTGAGGAGGTTTGTTCATCATGATTCACAAAGAAAGCGGGCTGTTATTCACAG	1020
D	b	982	GACCTTTGAGGAGGTTTGTTCATCATGATTCACAAAGAAAGCGGGCTGTTATTCACAG	1044
O	y	1019	TGAGGAGGAGAGCTGAGACCCCCCGCTGTGCACTGTGTGTTAAACACCCAGCCATCC	1077
D	b	1042	TGAGGAGGAGAGCTGAGACCCCCCGCTGTGCACTGTGTGTTAAACACCCAGCCATCC	1101
O	y	1079	TTCTCTTCAAAAGGATCTCTTCAATAGSAAACACTGAGAGGATTACTTGAAGAAATTTGG	1133
D	b	1102	TTCTCTTCAAAAGGAGATCTCTTCAATAGSAAACACTGAGAGGATTACTTGAAGAAATTTGG	1166
O	y	1139	ATTTCACCCCGGAAGATTTTATCAGCTTAACTCAGTAAATAATCATTTGAATAATTAAGT	1199

Db	1162	ATTCACCCGAGAAAGATTATTACACTTAACCTCAGATATAAATCATTTGAAGTAATAGCT	1221
Oy	1199	AAAAGCTAGTCTCTACACTTCCAGGCCCCAGCGCTCAAGTAATTTGAAATCTGCATTTACA	1258
Db	1222	AAAAGCTAGTCTCTACACTTCCAGGCCCCAGCGCTCAAGTAATTTGAAATCTGCATTTACA	1281
Oy	1259	GCTAGAGTAAACATACATTGTATGTCATGGAACAATGAGAGACAGTATTACAGTGTCTC	1318
Db	1282	GTTAGAGTAAACATATAATTGTATGATGGAACAATGAGAGAACATATTATACAGTGTCTC	1341
Oy	1319	CTACACCTTAATCAAGAAAGAAATTACAGACTGTGATTCTACAGTATGATTAATTTCT	1378
Db	1342	CTACACCTTAATCAAGAAAGAAATTACAGACTGTGATTCTACAGTATGATTAATTTCT	1401
Oy	1379	AAAAATGTTATCATTTAGGCGCTTTTGATTTTAAACCTTTGGGACTTATATCAAAATAT	1438
Db	1402	AAAAATGTTATCATTTAGGCGCTTTTGATTTTAAACCTTTGGGACTTATATCAAAATAT	1461
Oy	1439	GGTGTTATTTCTCCCTCCAGTTTCTGTGATATATTTGTTGATATTACATTTCTTGACTT	1498
Db	1462	GGTGTATTTCTCCCTCCAGTTTCTGTGATATATTTGTTGATATTACATTTCTTGACTT	1521
Oy	1489	ATATTTGAATGGTCTCTGTGTAAGAAAGAAATGATATATTTCTTGAAGACATCGATTTACA	1558
Db	1522	ATATTTGAATGGTCTCTGTGTAAGAAAGAAATGATATATTTCTTGAAGACATCGATTTACA	1581
Oy	1559	TTTATTTTACACTCTTATTTCTACATATGTAGAAGAAATGAGAGAAATGCCAATAATGTATGCT	1618
Db	1582	TTTATTTTACACTCTTATTTCTACATATGTAGAAGAAATGAGAGAAATGCCAATAATGTATGCT	1641
Oy	1619	GATATAAGTACGTGAAACAGAGATGTTGTGTCATGACAGCCCTTTGTTCTGTGGTGTCTCA	1678
Db	1642	GATATAAGTACGTGAAACAGAGATGTTGTGTCATGACAGCCCTTTGTTCTGTGGTGTCTCA	1701
Oy	1679	TGATCTCCCTCTAAGACATTTCCAACTTTAGCAACAGTATTACACTTTGTAAATTTGCA	1738
Db	1702	TGATCTCCCTCTAAGACATTTCCAACTTTAGCAACAGTATTACACTTTGTAAATTTGCA	1761
Oy	1739	AAGAAAGTTTCACTGTTATTTGAATACAGATATGCTTCACTGAAAAAACATATTCCTCAAA	1798
Db	1762	AAGAAAGTTTCACTGTTATTTGAATACAGATATGCTTCACTGAAAAAACATATTCCTCAAA	1821
Oy	1799	TAAATGAGAAATGTGTTGGCTCAGTACAGTACAGTCCAGAGGACAGTCACTTTTAAAGGTT	1858
Db	1822	TAAATGAGAAATGTGTTGGCTCAGTACAGTACAGTCCAGAGGACAGTCACTTTTAAAGGTT	1881
Oy	1859	GCGCTATTCACAGTAATCCGGGCGCTGTTTCCCGCTGGGCTCTCGGGCTGTCAAGCTTTTCCCT	1918
Db	1882	GCGCTATTCACAGTAATCCGGGCGCTGTTTCCCGCTGGGCTCTCGGGCTGTCAAGCTTTTCCCT	1941
Oy	1919	TTTCCATGTTGGTTGATTTCTCCTCAGGCTGTGAGCAAGTTCTGATCTTAATCCCAACA	1978
Db	1942	TTTCCATGTTGGTTGATTTCTCCTCAGGCTGTGAGCAAGTTCTGATCTTAATCCCAACA	2001
Oy	1979	CACGACAACTCCAGAAATTAAGTTCT 2005	
Db	2002	CACGACAACTCCAGAAATTAAGTTCT 2028	
RESULT 4			
AK000912			
LOCUS	AK000912	1674 bp	mRNA
DEFINITION	Homo sapiens cDNA FLJ10050 f1s, clone HEMBA1001257, highly similar	linear	PRI 01-AUG-2002
ACCESSION	AK000912		
VERSION	AK000912.1	GI:7021873	
KEYWORDS	oligo capping; f1s (full insert sequence);		
SOURCE	Homo sapiens embry, 10 weeks whole embryo, mainly head cDNA to		
	mRNA, clone_11b:HEMBA1 clone:HEMBA1001257.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiyama,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuno,Y. and Oshima,A., NEDO human cDNA sequencing project

TITLE Unpublished

JOURNAL 2 (bases 1 to 1674)

REFERENCE Isogai,T. and Otsuki,T.

AUTHORS Direct Submission

JOURNAL Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES
source location/Qualifiers
1..1674
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA100125"
/tissue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
/dev_stage="embryo, 10 weeks"
/note="cloning vector: PME18SFL3"

BASE COUNT 432 a 349 c 451 g 442 t

ORIGIN

Query Match 82.5%; Score 1653.2; DB 9; Length 1674;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1655; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGAGAGCTGTGGGCTGAAGGCTGCTCAGTTTCTTACGCGGGCACTGGGAA 60
DB 17 TTGAGAGCTGTGGGCTGAAGGCTGCTCAGTTTCTTACGCGGGCACTGGGAA 76
QY 61 GCGCATGAGCACTGAGGAGCATCTCGGTCGAGAGCTGTCCGGGCTGCGGCGCT 120
DB 77 GCGCATGAGCACTGAGGAGCATCTCGGTCGAGAGCTGTCCGGGCTGCGGCGCT 136
QY 121 TCTGTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 137 TCTGTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196
QY 181 CCCGCTACGAGCTGAGCGGCTGGGCGGGGCAAGCGCTGCTGCTGCTGCTGCTGCT 240
DB 197 CCCGCTACGAGCTGAGCGGCTGGGCGGGGCAAGCGCTGCTGCTGCTGCTGCTGCT 256
QY 241 AGCGGCGGAGCGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 257 AGCGGCGGAGCGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
QY 301 CTTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 317 CTTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
QY 361 ATCCGAAGGCTATTATGCGAGGCTGAGTGGATTTGGCCAGTCCAGAAAGCTTCCGCGGT 420
DB 377 ATCCGAAGGCTATTATGCGAGGCTGAGTGGATTTGGCCAGTCCAGAAAGCTTCCGCGGT 436
QY 421 TAGCTGCGCAGATATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 437 TAGCTGCGCAGATATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
QY 481 GTGTGGAATCCGTATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 497 GTGTGGAATCCGTATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
QY 541 TGTTGACATGCGGATTTATGCTTTTGTGACCGCAGCAGCAGCAGCAGGAGGCTCAGG 600

DB 557 TGTTGACATGCGGATTTATGCTTTTGTGACCGCAGCAGCAGCAGGAGGCTCAGG 616
QY 601 TCATTGATGCAAAATATGCTGGAAGAGCAGCATTTTAAAGTCTTTCTGTGAAAACTC 660
DB 617 TCATTGATGCAAAATATGCTGGAAGAGCAGCATTTTAAAGTCTTTCTGTGAAAACTC 676
QY 661 AGAAATGAGTCTGTGGGAAAGCACCTGAGAGCAGAAATGTTGATGTTGAGACACTT 720
DB 677 AGAAATGAGTCTGTGGGAAAGCACCTGAGAGCAGAAATGTTGATGTTGAGACACTT 736
QY 721 TCTATGAGCTTACAGACAGCAGATGGGAATTCATGCGCTGTTGGAGCAATAGAACCC 780
DB 737 TCTATGAGCTTACAGACAGCAGATGGGAATTCATGCGCTGTTGGAGCAATAGAACCC 796
QY 781 AGTCTACGAGCTCTGATCAAAAGAGCTTGAGTAAAGTGTGATGACTTCCCAATCAGA 840
DB 797 AGTCTACGAGCTCTGATCAAAAGAGCTTGAGTAAAGTGTGATGACTTCCCAATCAGA 856
QY 841 TGAGCATGATGATTTGGCCAGAAATGAAGAAGATTGAGATGTTTGCAGAAAGA 900
DB 857 TGAGCATGATGATTTGGCCAGAAATGAAGAAGATTGAGATGTTTGCAGAAAGA 916
QY 901 CGAAGCAGAGTGTGTCAAATCTTTACGCGCAGACAGATGCTGTGACTCCGGTTCTGA 960
DB 917 CGAAGCAGAGTGTGTCAAATCTTTACGCGCAGACAGATGCTGTGACTCCGGTTCTGA 976
QY 961 CTTTGGAGAGGTGTTTCATCATGATCACAACAAGAGAGGAGCTGTTATACACAGTG 1020
DB 977 CTTTGGAGAGGTGTTTCATCATGATCACAACAAGAGAGGAGCTGTTATACACAGTG 1036
QY 1021 AGAGCAGAGCTGAGCGCCCGCCCTGACCTCTGCTGTTTAAACCCAGCCATCCCTT 1080
DB 1037 AGAGCAGAGCTGAGCGCCCGCCCTGACCTCTGCTGTTTAAACCCAGCCATCCCTT 1096
QY 1081 CTTTCAAAAGGATCCTTTATAGAGACACACTGAGAGATCTGAGAAATTTGGAT 1140
DB 1097 CTTTCAAAAGGATCCTTTATAGAGACACACTGAGAGATCTGAGAAATTTGGAT 1156
QY 1141 TCAGCCGCGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAAAGTAA 1200
DB 1157 TCAGCCGCGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAAAGTAA 1216
QY 1201 AAGCTAGCTCTTAACCTTCCAGGCGCCAGGCTCAAGTGAATTTGATCTGATTTACAGT 1260
DB 1217 AAGCTAGCTCTTAACCTTCCAGGCGCCAGGCTCAAGTGAATTTGATCTGATTTACAGT 1276
QY 1261 GTGAGTAAACATTAATGATGATGATGAGAAACATGAGGAGACAGTATTAAGTCCCT 1320
DB 1277 GTGAGTAAACATTAATGATGATGATGAGAAACATGAGGAGACAGTATTAAGTCCCT 1336
QY 1321 ACCACTTAATCAAGAAAGAAATTAACAGACTTGATTTCAAGTATGATTTGAATTTAA 1380
DB 1337 ACCACTTAATCAAGAAAGAAATTAACAGACTTGATTTCAAGTATGATTTGAATTTAA 1396
QY 1381 AATGTTATCATTAAGGCTTTTATTAATAAATTTGGTACTTATTAATAATTTATG 1440
DB 1397 AATGTTATCATTAAGGCTTTTATTAATAAATTTGGTACTTATTAATAATTTATG 1456
QY 1441 TAGTTATTCGCTTCCAGTTGCTGATATTTGTTGATTAATAAATTTGATTAATAATTTATG 1500
DB 1457 TAGTTATTCGCTTCCAGTTGCTGATATTTGTTGATTAATAAATTTGATTAATAATTTATG 1516
QY 1501 AATTGTAATGGGTTCTAGTAAAGAAAGATATATTTCTGAAGACATGATATACATTT 1560
DB 1517 AATTGTAATGGGTTCTAGTAAAGAAAGATATATTTCTGAAGACATGATATACATTT 1576
QY 1561 TATTATACACTTGTATTTCTCAATGTAGAAATGAGAAATGCGCAAAATTTGATGTTGA 1620
DB 1577 TATTATACACTTGTATTTCTCAATGTAGAAATGAGAAATGCGCAAAATTTGATGTTGA 1636
QY 1621 TAAAGTCAGGTGAACAGAGTATTTGTTGATCCAG 1658

QY	1194	AAGGAAAAAGCTAGCTCTTAACCTCCAGGCCCCAGGGCCAGTGAATTTGAAATCTGAT	1253
Db	980	AAGGTAAAGCTAGTCTCTTAACCTCCAGGCCCCAGGGCTCAAGTGAATTTGAAATCTGAT	1039
QY	1254	TTACAGTGTAGAGTAPACACATTAATGTTGATGCATGAGAAACATGGAGAACGTAATTACA	1313
Db	1040	TTACAGTGTAGAGTAPACACATTAATGTTGATGCATGAGAAACATGGAGAACGTAATTACA	1099
QY	1314	GTGCTCTACCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTAACAGATGATTTGA	1373
Db	1100	GTGCTCTACCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTAACAGATGATTTGA	1159
QY	1374	ATTTCAAAAAATGGTTATCTATTAGGGCTTTTGATTTATTAACACTTTGGGTACTTATATCTAA	1433
Db	1160	ATTTCAAAAAATGGTTATCTATTAGGGCTTTTGATTTATTAACACTTTGGGTACTTATATCTAA	1219
QY	1434	ATTATGAGTAGTATTATTCTGCTCTCCAGTTTGCTTGATATATTTTGTGATATTTAAGATTCTT	1493
Db	1220	ATTATGAGTAGTATTATTCTGCTCTCCAGTTTGCTTGATATATTTTGTGATATTTAAGATTCTT	1279
QY	1494	GACTATATATTTTGAATGGGTTCTAGTGAAGAAAAGAAATGATATATCTTGAAGACATCGAT	1553
Db	1280	GACTATATATTTTGAATGGGTTCTAGTGAAGAAAAGAAATGATATATCTTGAAGACATCGAT	1339
QY	1554	ATACATTTTATTTTACACTCTTGATTTCTACATGTTAGAAAATGAGAAATGCCACAAATTTGT	1613
Db	1340	ATACATTTTATTTTACACTCTTGATTTCTACATGTTAGAAAATGAGAAATGCCACAAATTTGT	1399
QY	1614	ATGGGATAAAAAGTACGTGAAGAACAGAGTGAATGGTTCATCAGAGCCCTTTTGCTTGCT	1673
Db	1400	ATGGGATAAAAAGTACGTGAAGAACAGAGTGAATGGTTCATCAGAGCCCTTTTGCTTGCTTGCT	1459
QY	1674	GTTCTATGATTCCTCTTACAGACATTTCCAAACTTTAGCAACAGTTATACACACTTTGTAT	1733
Db	1460	GTTCTATGATTCCTCTTACAGACATTTCCAAACTTTAGCAACAGTTATATACACTTTGTAT	1519
QY	1734	TTTGCAAAAAAGTTTCACTCGTATTTGAATCAGATGGCTTCACAGTGAAGAAAACATATAC	1793
Db	1520	TTTGCAAAAAAGTTTCACTCGTATTTGAATCAGATGGCTTCACAGTGAAGAAAACATATAC	1579
QY	1794	CAAAATTAATGAGGAATGTGTTGGCTCACTACGTAGAGTCCAGAGGAGCAGTCAAGTTTAA	1853
Db	1580	CAAAATTAATGAGGAATGTGTTGGCTCACTACGTAGAGTCCAGAGGAGCAGTCAAGTTTAA	1639
QY	1854	GGGTGGCTCTGATTCACAGTAACCTGGGGGGCTGTGTTCCCGTGGGTCTGTGGGTCTGACGT	1913
Db	1640	GGGTGGCTCTGATTCACAGTAACCTGGGGGGCTGTGTTCCCGTGGGTCTGTGGGTCTGACGT	1699
QY	1914	TTTCCTTTCTCATGCTGTTTGGATTTTCTCCCTCAGAGGCTGTAGCAAGTTCGGATCTTATACC	1973
Db	1700	TTTCCTTTCTCATGCTGTTTGGATTTTCTCCCTCAGAGGCTGTAGCAAGTTCGGATCTTATACC	1759
QY	1974	CAACACACAGCAACATCCAGAAATTAAGTTCT 2005	
Db	1760	CAACACACAGCAACATCCAGAAATTAAGTTCT 1791	
RESULT 6			
AXI06326			
LOCUS	AXI06326	1621 bp	DNA linear PAT 30-APR-2001
DEFINITION	Sequence 107 from Patent WO0125272.		
ACCESSION	AXI06326		
VERSION	AXI06326.1	GI:13922012	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1. (bases 1 to 1621)		
	Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.		
	Compositions and methods for therapy and diagnosis of prostate		
	cancer		
JOURNAL	Patent: WO 0125272-A 107 12-APR-2001;		

CORIXA CORPORATION (US)									
FEATURES	Source	Location/Qualifiers							
		1. 1621							
		/organism="Homo sapiens"							
		/db_xref="taxon:9606"							
BASE COUNT	461 a	330 c	412 g	418 t					
ORIGIN									
Query Match	78.5%	Score 1574.2;	DB 6;	Length 1621;					
Best Local Similarity	99.8%	Pred. No. 0;							
Matches 1576;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps		
OY	62	CGCCATGCGACATGCAAGGCGATCTCGGTGCTGAGACTGTCCGGCTGGCCCGGCGCGCTT	121						
Db	1	CGCCATGCGACTGCAAGGCGATCTCGGTATGAGACTGTCCGGCTGGCCCGGCGCGCTT	60						
OY	122	CTGTCTATGTGCTTCCTGCTGCTGACTTGTGGGGCCGCTGTGGTACCGCGTGAACCGGCGCGGCTC	181						
Db	61	CTGTCTATGTGCTTCCTGCTGCTGACTTGTGGGGCCGCTGTGTGACCGGTGAACCGGCGCGGCTC	120						
OY	182	CCGCTACGACAGCGACCGCTGTGGGCCGGGGGCAAGCGCTCGCTAGTGTGAGACTTGACA	241						
Db	121	CCGCTACGACAGCGACCGCTGTGGGGCCGGGGGCAAGCGCTCGCTAGTGTGAGACTTGACA	180						
OY	242	GCCGGGGGAGCCCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTCTGGAGCC	301						
Db	181	GCCGGGGGAGCCCGCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTCTGGAGCC	240						
OY	302	CTTCCGCGCGGCTGTGATGAGAGAACTCAGCTGGGGCCAGAGATTCTGCACGGGGAAAA	361						
Db	241	CTTCCGCGCGGCTGTGATGAGAGAACTCAGCTGGGGCCAGAGATTCTGCACGGGGAAAA	300						
OY	362	TCCAAAGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAGACTTCTGCCGGTT	421						
Db	301	TCCAAAGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGAGACTTCTGCCGGTT	360						
OY	422	AGCTGGCAAGATATCAACTATTGGCTTTGTCAGGTGTTCTCTGAAAAATTGGCAGAAG	481						
Db	361	AGCTGGCAAGATATCAACTATTGGCTTTGTCAGGTGTTCTCTGAAAAATTGGCAGAAG	420						
OY	482	TGGTGAAGATTCGTAATGCCCGCCGCTGAATCTCTGGCTGACTTTGTGTGTGGCCCTTAT	541						
Db	421	TGGTGAAGATTCGTAATGCCCGCCCGCTGAATCTCTGGCTGACTTTGTGTGTGGCCCTTAT	480						
OY	542	GTTGTCACTGGGCATTATTAATGGGCTTTTTCACCGCAAGCACTGGCAAGGGTCAAGT	601						
Db	481	GTTGTCACTGGGCATTATTAATGGGCTTTTTCACCGCAAGCACTGGCAAGGGTCAAGT	540						
OY	602	CATTGATGCAAAATATGTGTGAAGAGAAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA	661						
Db	541	CATTGATGCAAAATATGTGTGAAGAGAAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA	600						
OY	662	GAATTCGAGTCTGTGGGAAGCACCTCGAGAGACAGAAATGTTGGATGTTGGAGCACCTTT	721						
Db	601	GAATTCGAGTCTGTGGGAAGCACCTCGAGAGACAGAAATGTTGGATGTTGGAGCACCTTT	660						
OY	722	CTATCGACTTACAGACAGAGATGGGGAAATTCATGGCTGTTTGGAGCAATGAACCCCA	781						
Db	661	CTATCGACTTACAGACAGAGATGGGGAAATTCATGGCTGTTTGGAGCAATGAACCCCA	720						
OY	782	GTTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAAGTCCCAATCAGAT	841						
Db	721	GTTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAAGTCCCAATCAGAT	780						
OY	842	GAGCATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAAAGAGC	901						
Db	781	GAGCATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAAAGAGC	840						
OY	902	GAAGCAGAGTGTGTCAAAATCTTTGAGGGCCACATGGCTGTGACATCCGGTCTGTGAC	961						
Db	841	GAAGCAGAGTGTGTCAAAATCTTTGAGGGCCACATGGCTGTGACATCCGGTCTGTGAC	900						
OY	962	TTTTAGGAGGTTTGTTCATCATGATCACAAAGAGCGGGCTGTTTATCAGCAGTGA	1021						

Db	901	TTTTGAGGAGTTGTTTCATCATGATCATCAACAAAGAAAGGCGGCTCCTTTATCACAGTA	960
Qy	1022	GGAGCAGAGAGCTGACGCCCCCGCCGCAACCTGCTGTTAAACACCCCGCATCCCTTC	1081
Db	961	GGAGCAGAGAGTBAAGCCCGCCGCTGACCTGCTGTTAAACACCCCGCATCCCTTC	1020
Qy	1082	TTTTCAAAAGGAGTCCCTTTCATATGAGAACACACTGAGAGATATCTTGAAATTTGGATT	1141
Db	1021	TTTTCAAAAGGAGTCCCTTTCATATGAGAACACACTGAGAGATATCTTGAAATTTGGATT	1080
Qy	1142	CACGCCGGAAGATTTATCAGCTTAATCAGATAAATCATTTGAAAGTAAATAGTAAA	1201
Db	1081	CACGCCGGAAGATTTATCAGCTTAATCAGATAAATCATTTGAAAGTAAATAGTAAA	1140
Qy	1202	AGCTAGTCTTAATCTTCCAGGCCCCAGGCTCAAGTGAAATTTGAAATCTGATTTACAGTG	1261
Db	1141	AGCTAGTCTTCTAACTTCCAGGCCCCAGGCTCAAGTGAAATTTGAAATCTGATTTACAGTG	1200
Qy	1262	TAGAGTAAACAATTAATCATTTGATGATGAGAAACATGAGAGAACAGATTTACAGTGCTTA	1321
Db	1201	TAGAGTAAACAATTAATCATTTGATGATGAGAAACATGAGAGAACAGATTTACAGTGCTTA	1260
Qy	1322	CCACTCATTAACAAGAAAGAAATTAACAGACTGTGTTCTCAAGATGATGATTAATCTTAAA	1381
Db	1261	CCACTCATTAACAAGAAAGAAATTAACAGACTGTGTTCTCAAGATGATGATTAATCTTAAA	1320
Qy	1382	AATGGTATTCATTAAGGCTTTGATTTATTAACCTTGGGTACTGTTACTAAATATATGCT	1441
Db	1321	AATGGTATTCATTAAGGCTTTGATTTATTAACCTTGGGTACTGTTACTAAATATATGCT	1380
Qy	1442	AGTTATTTTCGCTTCGACGTTTGCTTGATATATTTGTTGATATTAGATTTCTGACTTAA	1501
Db	1381	AGTTATTTTCGCTTCGACGTTTGCTTGATATATTTGTTGATATTAGATTTCTGACTTAA	1440
Qy	1502	TTTTGAATGGGTTCTATGTAAGAAAGAAATGATATTTCTTGAAGATCATGATATACATTT	1561
Db	1441	TTTTGAATGGGTTCTATGTAAGAAAGAAATGATATTTCTTGAAGATCATGATATACATTT	1500
Qy	1562	ATTTACACTCTTGATTTCTACAATGATAGAAATGAGAAATGCCCAAAATTTGATGGTAT	1621
Db	1501	ATTTACACTCTTGATTTCTACAATGATAGAAATGAGAAATGCCCAAAATTTGATGGTAT	1560
Qy	1622	AAAAGTCACGTGAACAGTA 1640	
Db	1561	AAAAGTCACGTGAACAAAA 1579	
RESULT 7			
LOCUS	AX140617	1621 bp	DNA
DEFINITION	Sequence 107 from Patent WO0134802.		Linear
ACCESSION	AX140617		
VERSION	AX140617.1	GI:14280735	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 1621)		
AUTHORS	Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Reed, S. G., Kalos, M. D., Retter, M. W., Stolk, J. A., Day, C. H., Skelky, J. A. and Wang, A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0134802-A 107 17-MAY-2001;		
FEATURES	CORLXA CORPORATION (US)		
source	Location/Qualifiers		
	1..1621		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	461 a	330 c	412 g 418 t
ORIGIN			

QY 1082 TTTCAAAAGGATCTTTCTTAGAGACACACTGAGGAGATCTTGAGAAATTTGGATT 1141
 |||||||
 Db 1021 TTTCAAAAGGATCTTTCTTAGAGAACACACTGAGGAGATCTTGAGAAATTTGGATT 1080
 |||||||
 QY 1142 CAGCCGGAAGAGATTATAGCTTAACATGATTAAGTAAATAGTAAAGTAA 1201
 |||||||
 Db 1081 CAGCCGGAAGAGATTATAGCTTAACATGATTAAGTAAATAGTAAAGTAA 1140
 |||||||
 QY 1202 AGCTAGCTCTAATCTCCAGGCCACGAGCTCAAGTAAATTTGAATCTGATTTACAGTG 1261
 |||||||
 Db 1141 AGCTAGCTCTAATCTCCAGGCCACGAGCTCAAGTAAATTTGAATCTGATTTACAGTG 1200
 |||||||
 QY 1262 TAGAGTACACATTAATCTTATAGCATGAGAAATAGGAGACAGTATTACAGTGCTTA 1321
 |||||||
 Db 1201 TAGAGTACACATTAATCTTATAGCATGAGAAATAGGAGACAGTATTACAGTGCTTA 1260
 |||||||
 QY 1322 CCACTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTAGTATGATTAAGTAAATCTTAA 1381
 |||||||
 Db 1261 CCACTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTAGTATGATTAAGTAAATCTTAA 1320
 |||||||
 QY 1382 AATGTTATCATTAAGGCTTTGATTTATTAACCTTTGGTACTTAATTAATTAATGAT 1441
 |||||||
 Db 1321 AATGTTATCATTAAGGCTTTGATTTATTAACCTTTGGTACTTAATTAATTAATGAT 1380
 |||||||
 QY 1442 AGTTATCTGCTCTCCAGCTTTGCTGATATATTTGATATTAAGTATTCTGACTTATA 1501
 |||||||
 Db 1381 AGTTATCTGCTCTCCAGCTTTGCTGATATATTTGATATTAAGTATTCTGACTTATA 1440
 |||||||
 QY 1502 TTTTGAATGGGTTCTAGTAAAGAAAGATATATTTCTTGAAGACATGATATACATT 1561
 |||||||
 Db 1441 TTTTGAATGGGTTCTAGTAAAGAAAGATATATTTCTTGAAGACATGATATACATT 1500
 |||||||
 QY 1562 ATTATACCTCTTATCTTACATATGTAGAAAATGAGAAATGCCAATTTGTATGTGAT 1621
 |||||||
 Db 1501 ATTATACCTCTTATCTTACATATGTAGAAAATGAGAAATGCCAATTTGTATGTGAT 1560
 |||||||
 QY 1622 AAAAGTCAGCTGAACAGA 1640
 |||||||
 Db 1561 AAAAGTCAGCTGAACAAA 1579
 |||||||

RESULT 8
 AX200477 1621 bp DNA linear PAT 29-AUG-2001
 LOCUS AX200477
 DEFINITION Sequence 107 from Patent W00151633.
 ACCESSION AX200477
 VERSION AX200477.1 GI:15390290
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1621)
 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
 Stolk,J.A., Skeiky,Y.A., Wang,A. and Weaghter,M.J.
 TITLE Compositions and methods for the therapy and diagnosis of prostate
 cancer
 JOURNAL Patent: WO 0151633-A 107 19-JUL-2001;
 CORIXA CORPORATION (US)
 FEATURES
 source 1..1621
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 461 a 330 c 412 g 418 t
 ORIGIN
 Query Match 78.5%; Score 1574.2; DB 6; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 62 CGCGATGACACTGACGAGATCTGCTGAGAGCTGTCCGGCTGGCCCCGGCGCTT 121
 |||||||

Db 1 CGCCATGACACTGACGAGGATCTCGGTCAATGAGCTGTCCGGCTGGCCCCGGCGCTT 60
 |||||||
 QY 122 CTGTGATATGCTCTGCTGACTTCCGGGGCCCTGTGTACGCGGTGACCGCCGGCTC 181
 |||||||
 Db 61 CTGTGATATGCTCTGCTGACTTCCGGGGCCCTGTGTGTACGCGGTGACCGCCGGCTC 120
 |||||||
 QY 182 CGCGTACAGCTGAGCGCGCTTGGGGCCGGGCAAGCGCTGCTGTGTGACTGAGCA 241
 |||||||
 Db 121 CGCGTACAGCTGAGCGCGCTTGGGGCCGGGCAAGCGCTGCTGTGTGACTGAGCA 180
 |||||||
 QY 242 GCGCGGGGAGCGCGCGCTGTGCGGGCTGTGCAAGCGGTGAGTGTGCTGTGAGCC 301
 |||||||
 Db 181 GCGCGGGGAGCGCGCGCTGTGCGGGCTGTGCAAGCGGTGAGTGTGCTGTGAGCC 240
 |||||||
 QY 302 CTTCGCGCGGCTGTATGAGGAAATCCAGCTGGGCCAGAGATTTCTGCAGCGGAAAA 361
 |||||||
 Db 241 CTTCGCGCGGCTGTATGAGGAAATCCAGCTGGGCCAGAGATTTCTGCAGCGGAAAA 300
 |||||||
 QY 362 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGCTT 421
 |||||||
 Db 301 TCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGCTT 360
 |||||||
 QY 422 AGCTGGCCAGATATCACTAATTTGGCTTTGTACGGTGTCTCAAAAATTTGGCAGAG 481
 |||||||
 Db 361 AGCTGGCCAGATATCACTAATTTGGCTTTGTACGGTGTCTCAAAAATTTGGCAGAG 420
 |||||||
 QY 482 TGGTGAAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTGTGTGTGCTTAT 541
 |||||||
 Db 421 TGGTGAAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTGTGTGTGCTTAT 480
 |||||||
 QY 542 GTGTGACATGGGATTTATATGCTCTTTTGAACCCACACGACATGGCAAGGTGAGGT 601
 |||||||
 Db 481 GTGTGACATGGGATTTATATGCTCTTTTGAACCCACACGACATGGCAAGGTGAGGT 540
 |||||||
 QY 602 CATTGATGCAATATATGTTGGAAGAAACAGCATTTTAAGTTCTTTCTGTGAAAACTCA 661
 |||||||
 Db 541 CATTGATGCAATATATGTTGGAAGAAACAGCATTTTAAGTTCTTTCTGTGAAAACTCA 600
 |||||||
 QY 662 GAAATGAGTCTGTGGAGAACACCTTGAGGACAGAAATGTTGATGTGTGAGCACCTTT 721
 |||||||
 Db 601 GAAATGAGTCTGTGGAGAACACCTTGAGGACAGAAATGTTGATGTGTGAGCACCTTT 660
 |||||||
 QY 722 CTATACGACTTACAGACAGACATGGGAAATCAATGGCTTGGAGCAATGAAACCCCA 781
 |||||||
 Db 661 CTATACGACTTACAGACAGACATGGGAAATCAATGGCTTGGAGCAATGAAACCCCA 720
 |||||||
 QY 782 GTTCTACGAGCTCTGATCAAAAGAGACTTGACTAAAGTGTGATGAATCTCCCAATCAGAT 841
 |||||||
 Db 721 GTTCTACGAGCTCTGATCAAAAGAGACTTGACTAAAGTGTGATGAATCTCCCAATCAGAT 780
 |||||||
 QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAAGAGAC 901
 |||||||
 Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAAGAGAC 840
 |||||||
 QY 902 GAAGGAGAGTGTGTCAAAATCTTTACGCGCACAGATGCCGTGTGTACCTCCGTTGTGAC 961
 |||||||
 Db 841 GAAGGAGAGTGTGTCAAAATCTTTACGCGCACAGATGCCGTGTGTACCTCCGTTGTGAC 900
 |||||||
 QY 962 TTTTGAAGAGTTGTCATCATGATCAACAACAAGAGAGGCGCTTTATACACAGTAA 1021
 |||||||
 Db 901 TTTTGAAGAGTTGTCATCATGATCAACAACAAGAGAGGCGCTTTATACACAGTAA 960
 |||||||
 QY 1022 GAGACAGAGAGTGAAGCCCGCCCTGACCTGCTGTAAACACCCACGATCCCTTC 1081
 |||||||
 Db 961 GAGACAGAGAGTGAAGCCCGCCCTGACCTGCTGTAAACACCCACGATCCCTTC 1020
 |||||||
 QY 1082 TTTCAAAAGGATCTTTCTTAGAGACACACTGAGGAGATCTTGAGAAATTTGGATT 1141
 |||||||
 Db 1021 TTTCAAAAGGATCTTTCTTAGAGAACACACTGAGGAGATCTTGAGAAATTTGGATT 1080
 |||||||
 QY 1142 CAGCCGGAAGAGATTATAGCTTAACATGATTAAGTAAATAGTAAAGTAA 1201
 |||||||
 Db 1081 CAGCCGGAAGAGATTATAGCTTAACATGATTAAGTAAATAGTAAAGTAA 1140
 |||||||

QY 1202 AGCTAGCTCTACTCTCCAGGCCCGCCAGCTCAAGTGAATTTGAATACATTCATTTACAGTG 1261
|||||
Db 1141 AGCTAGCTCTACTCTCCAGGCCCGCCAGCTCAAGTGAATTTGAATACATTTACAGTG 1200
QY 1262 TAGAGTACACATACATTTGATGATGAGAAACATGGAGACATGATTTACAGTCTCTA 1321
|||||
Db 1201 TAGAGTACACATACATTTGATGATGAGAAACATGGAGACATGATTTACAGTCTCTA 1260
QY 1322 CCACCTCAATCAAGAAAGAAATTTACAGCTCTGATTTCTACAGTATGATTTGAATTTCTAA 1381
|||||
Db 1261 CCACCTCAATCAAGAAAGAAATTTACAGCTCTGATTTCTACAGTATGATTTGAATTTCTAA 1320
QY 1382 AATGTTATCATATAGAGCTTTTGTATTTAAACCTTTGGTACTTCTTACTAAATTTAGT 1441
|||||
Db 1321 AATGTTATCATATAGAGCTTTTGTATTTAAACCTTTGGTACTTCTTACTAAATTTAGT 1380
QY 1442 AGTTATTTCTGCTCCAGTTTGTGATATATTTGTTGATATTTAAATTTCTGACTTATA 1501
|||||
Db 1381 AGTTATTTCTGCTCCAGTTTGTGATATATTTGTTGATATTTAAATTTCTGACTTATA 1440
QY 1502 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATATTTCTGAGACATGATATATCATTT 1561
|||||
Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATATTTCTGAGACATGATATATCATTT 1500
QY 1562 ATTTCACCTCTGATTTCTACATGATGAGAAATGAGAAATGCCACAAATTTGATGAT 1621
|||||
Db 1501 ATTTCACCTCTGATTTCTACATGATGAGAAATGAGAAATGCCACAAATTTGATGAT 1560
QY 1622 AAAAGTCAGCTGAACACGA 1640
|||||
Db 1561 AAAAGTCAGCTGAACACGA 1579

RESULT 9
AX267133
LOCUS AX267133 107 bp DNA 1linear PAT 26-Oct-2001
DEFINITION Sequence 107 from Patent WO01/3032.
ACCESSION AX267133
VERSION AX267133.1 GI:16515918
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalsb,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedlick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITL Composition and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 01/3032-A 107 04-Oct-2001;
FEATURES
source CORIAX CORPORATION (US)
location/Qualifiers
1..1621
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN
Query Match 78 5%; Score 1574.2; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred No 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 182 CCGCTAGACAGTACAGCGCTTGCGCGCGGCGCAAGCGCTCCGCTAGCTGAGCTGAACGA 241
|||||
Db 121 CCGCTAGACAGTACAGCGCTTGCGCGCGGCGCAAGCGCTCCGCTAGCTGAGCTGAACGA 180
QY 242 GCGCGGGGAGCGCGCGCTGCGCGCTGCTGTGTGCAAGCGCTCGGATGTGCTGTGAGGC 301
|||||
Db 181 GCGCGGGGAGCGCGCGCTGCGCGCTGCTGTGTGCAAGCGCTCGGATGTGCTGTGAGGC 240
QY 302 CTTCCGCGCGGCTGTGATGGAAGAACTCCAGCTGGGCGCAGAGATTTCTGCACGGGAAA 361
|||||
Db 241 CTTCCGCGCGGCTGTGATGGAAGAACTCCAGCTGGGCGCAGAGATTTCTGCACGGGAAA 300
QY 362 TCCAGGCTTATTTATGCGAGGCTAGTGATTTGGCAGTCAAGAGCTTCTGCGGTT 421
|||||
Db 301 TCCAGGCTTATTTATGCGAGGCTAGTGATTTGGCAGTCAAGAGCTTCTGCGGTT 360
QY 422 AGCTGGCCAGATATCAATATTTGCTTTGTCTCAGAGTCTCTCAAAAATTGGCAGAG 481
|||||
Db 361 AGCTGGCCAGATATCAATATTTGCTTTGTCTCAGAGTCTCTCAAAAATTGGCAGAG 420
QY 482 TGTGGAATCCGATATGCCCGCGTGAATCTGCTGAGCTTTGCTGTGTGTGAGCTTAT 541
|||||
Db 421 TGTGGAATCCGATATGCCCGCGTGAATCTGCTGAGCTTTGCTGTGTGTGAGCTTAT 480
QY 542 GTGTGACCTGGGATTTATATGCTCTTTTGACCGACACAGGAGTGGCAAGTCCAGT 601
|||||
Db 481 GTGTGACCTGGGATTTATATGCTCTTTTGACCGACACAGGAGTGGCAAGTCCAGT 540
QY 602 CATGTATGCAAAATATGTTGGAGAGAAAGCATATTTAAGTCTTTCTGTGAAAACTCA 661
|||||
Db 541 CATGTATGCAAAATATGTTGGAGAGAAAGCATATTTAAGTCTTTCTGTGAAAACTCA 600
QY 662 GAAATGAGTCTGTGGGAAGCACTGCGAGACAGACATGTTGGATGTGTGAGCACCTTT 721
|||||
Db 601 GAAATGAGTCTGTGGGAAGCACTGCGAGACAGACATGTTGGATGTGTGAGCACCTTT 660
QY 722 CTATAGACCTTACAGACAGACAGATGGGAAATTCATGCTGTGTGAGCAATAGAACCCA 781
|||||
Db 661 CTATAGACCTTACAGACAGACAGATGGGAAATTCATGCTGTGTGAGCAATAGAACCCA 720
QY 782 GTTCTACGAGCTCTGATCAAGAGACTTGACTAAGTCTGATGAACCTTCCCATTCAGAT 841
|||||
Db 721 GTTCTACGAGCTCTGATCAAGAGACTTGACTAAGTCTGATGAACCTTCCCATTCAGAT 780
QY 842 GAGCATGATGATTTGGCCAGAAATGAGAAAGATTTGCAAGATGATTTTGCAAAAGAAC 901
|||||
Db 781 GAGCATGATGATTTGGCCAGAAATGAGAAAGATTTGCAAGATGATTTTGCAAAAGAAC 840
QY 902 GAAGCAGAGTGTGTCAATCTTTGACGCGACAGATGCTGTGTGACTCCGTTCTGAC 961
|||||
Db 841 GAAGCAGAGTGTGTCAATCTTTGACGCGACAGATGCTGTGTGACTCCGTTCTGAC 900
QY 962 TTTTGAAGAGTGTTCATCATGATCACAACAGAAAGGAGGCGCTTTATCACAGTGA 1021
|||||
Db 901 TTTTGAAGAGTGTTCATCATGATCACAACAGAAAGGAGGCGCTTTATCACAGTGA 960
QY 1022 GGAGCAGAGATGAGGCGCGCGCTGCGACCTGCTGTAAACACCGCAGCATCCCTTC 1081
|||||
Db 961 GGAGCAGAGATGAGGCGCGCGCTGCGACCTGCTGTAAACACCGCAGCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTATAGAGAAACACAGTGAAGATTAAGTGAATTTGAGAT 1141
|||||
Db 1021 TTTCAAAAGGATCTTTATAGAGAAACACAGTGAAGATTAAGTGAATTTGAGAT 1080
QY 1142 CAGCGCGGAAGATTTATCAGCTTAACATCAGATTAATCATTTGAAGATTAAGTGA 1201
|||||
Db 1081 CAGCGCGGAAGATTTATCAGCTTAACATCAGATTAATCATTTGAAGATTAAGTGA 1140
QY 1202 AGCTAGTCTTAACCTTCAGGCGCCAGGCTCAAGTGAATTTGAATTAAGTCAAGTG 1261
|||||
Db 1141 AGCTAGTCTTAACCTTCAGGCGCCAGGCTCAAGTGAATTTGAATTAAGTCAAGTG 1200
QY 1262 TAGAGTACACATACATTTGATGATGAGAAACATGGAGACATGATTTACAGTCTCTA 1321

```

|||||
Db 1201 TAGGTACACATATACATGATGATGAGAAACATGAGGAACGATATTACAGTGTCTTA 1260
QY 1322 CCACCTAATCAAGAAAGAAATTCACAGCTCTGATTCACAGTATGATTAATCTTAA 1381
Db 1261 CCACCTAATCAAGAAAGAAATTCACAGCTCTGATTCACAGTATGATTAATCTTAA 1320
QY 1382 AATGGTATATCATATGAGGCTTTGATTTATATAAACTTGGGACTTATACATAATATGCT 1441
Db 1321 AATGGTATATCATATGAGGCTTTGATTTATATAAACTTGGGACTTATACATAATATGCT 1380
QY 1442 AGTATCTGCTCCAGTCTGCTGATATATTTGATATTTAGATTTCTGACTATA 1501
Db 1381 AGTATCTGCTCCAGTCTGCTGATATATTTGATATTTAGATTTCTGACTATA 1440
QY 1502 TTTTGATGGGTTCTAGTGAAGAAAGATGATATTTCTGAGACATCGATATACATTT 1561
Db 1441 TTTTGATGGGTTCTAGTGAAGAAAGATGATATTTCTGAGACATCGATATACATTT 1500
QY 1562 ATTTACACTCTTGTATCTACATGTAGAAAATGAGAAATGCCAAATTTGATGTGAT 1621
Db 1501 ATTTACACTCTTGTATCTACATGTAGAAAATGAGAAATGCCAAATTTGATGTGAT 1560
QY 1622 AAAAGTCACGTGGAACAGA 1640
Db 1561 AAAAGTCACGTGGAACAAA 1579

RESULT 10
AC008954 90111 bp DNA linear PRI 08-JUN-2001
LOCUS AC008954 Homo sapiens chromosome 5 clone CTD-2340N2, complete sequence.
DEFINITION AC008954 AC008954.6 GI:14329063
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 90111)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 90111)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 90111)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (27-APR-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 90111)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:13811891.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.1.
SFS Content:
SHGC-56588 G36925
WI-856 G02835
SHGC-36018 G30037.
FEATURES
source location/Qualifiers
1. 90111
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

/chromosome="5"
/clone="CTD-2340N2"
BASE COUNT 25692 a 18129 c 18543 g 27747 t
ORIGIN
Query Match 59.9%; Score 1201.4; DB 9; Length 90111;
Best Local Similarity 99.9%; Pred. No. 2.1e-263;
Matches 1202; Conservatve 0; Mismatches 1; Indels 0; Gaps 0;
QY 803 AGCACTTGACATAAGTCTGATGAACTTCCCAATCATGATGAGCATGATGGCCAGA 862
Db 4136 AGCACTTGACATAAGTCTGATGAACTTCCCAATCATGATGAGCATGATGGCCAGA 41695
QY 863 AATGAGAAGAAAGTTGCGAGATGATTTGCAAAAGACGAGAGGAGGTGCTCAAT 922
Db 41696 AATGAGAAGAAAGTTGCGAGATGATTTGCAAAAGACGAGAGGAGGTGCTCAAT 41755
QY 923 CTTGAGGCGACAGATCCCTGCTGACTCCCGGTTCTACCTTTGAGAGAGTTGCTATCA 982
Db 41756 CTTGAGGCGACAGATCCCTGCTGACTCCCGGTTCTACCTTTGAGAGAGTTGCTATCA 41815
QY 983 TGATCACAACAGAGAGGCGCTGCTTTATCACCAGTGAAGAGAGAGAGAGAGAGAGAG 1042
Db 41816 TGATCACAACAGAGAGGCGCTGCTTTATCACCAGTGAAGAGAGAGAGAGAGAGAGAG 41875
QY 1043 CCTGCACTCTGCTGTTTAAACACCCAGCCATCCCTTTTCAAAAGGATCCTTTCAT 1102
Db 41876 CCTGCACTCTGCTGTTTAAACACCCAGCCATCCCTTTTCAAAAGGATCCTTTCAT 41935
QY 1103 AGGAGAACACACAGTGAAGATCTTGAAGATTTGGATTCAGCCGCCAAGAGATTTTCA 1162
Db 41936 AGGAGAACACACAGTGAAGATCTTGAAGATTTGGATTCAGCCGCCAAGAGATTTTCA 41995
QY 1163 GCTTAACCTCAGATTAATATCTTGAAGATTAATTAAGTAAAGCTGATCTTAACCTCAGG 1222
Db 41996 GCTTAACCTCAGATTAATATCTTGAAGATTAATTAAGTAAAGCTGATCTTAACCTCAGG 42055
QY 1223 CCCAGGCTCAAGTGAATTTGAATATGCAATTTACAGTGAAGATTAACATTAACATTTGT 1282
Db 42056 CCCAGGCTCAAGTGAATTTGAATATGCAATTTACAGTGAAGATTAACATTAACATTTGT 42115
QY 1283 ATGATGGAACATGAGAGAGAGAGAGATTTACAGATCTTACACCTCTAATCAAGAAAGAA 1342
Db 42116 ATGATGGAACATGAGAGAGAGAGAGATTTACAGATCTTACACCTCTAATCAAGAAAGAA 42175
QY 1343 TTACAGACTGATTTACAGAGTGAATGATTAATCTTAAATGGTTATTAAGAGGCTTT 1402
Db 42176 TTACAGACTGATTTACAGAGTGAATGATTAATCTTAAATGGTTATTAAGAGGCTTT 42235
QY 1403 TGATTTTAAACCTTGGGACTTATATCTAATTAATGATGATTTGCTGCCCTTCCAGTTT 1462
Db 42236 TGATTTTAAACCTTGGGACTTATATCTAATTAATGATGATTTGCTGCCCTTCCAGTTT 42295
QY 1463 GCTTGATATATTTGTTGATATTAAGATTTCTTGACTTATATTTGATAGGGTTGAGGAA 1522
Db 42296 GCTTGATATATTTGTTGATATTAAGATTTCTTGACTTATATTTGATAGGGTTGAGGAA 42355
QY 1523 AAAGAGATGATATTTCTTGAAGACATGATATCAATTTATTTTACACTCTTGATTTTACA 1582
Db 42356 AAAGAGATGATATTTCTTGAAGACATGATATCAATTTATTTTACACTCTTGATTTTACA 42415
QY 1583 ATGTGAAAAATGAGAAATGCCACAAATTTATGATGATTAAGTACGTAAGACAGAGT 1642
Db 42416 ATGTGAAAAATGAGAAATGCCACAAATTTATGATGATTAAGTACGTAAGACAGAGT 42475
QY 1643 GATTGGTTGATCAGAGGCTTTTGTCTTGAGTTTCAATGATCTCCCTTAAGACATTTCCA 1702
Db 42476 GATTGGTTGATCAGAGGCTTTTGTCTTGAGTTTCAATGATCTCCCTTAAGACATTTCCA 42535
QY 1703 AACTTTAGCAAGATTATCACACTTTGATTTGCAAAAGAAAGTTTACACTGATTTGAA 1762
Db 42536 AACTTTAGCAAGATTATCACACTTTGATTTGCAAAAGAAAGTTTACACTGATTTGAA 42595

```



```

Db      7260  CAGCGTGGAGCAACTTCTGATCTTATACCCACACACAGCAACATCCAGAAATTAAGA 7319
OY      2003  TCT 2005
Db      7320  TCT 7322

RESULT 12
AC026707      155013 bp      DNA      linear      HTG 07-MAR-2002
LOCUS      AC026707
DEFINITION      Homo sapiens chromosome 5 clone CTD-2075C7, WORKING DRAFT SEQUENCE,
2 Ordered pieces.
AC026707
AC026707.5 GI:19224781
HTG: HTGS-PHASE2: HTGS-DRAFT; HTGS-ACTIVEFIN.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 155013)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 5
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 155013)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Direct Submission
REFERENCE      3 (bases 1 to 155013)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT      On Mar 7, 2002 this sequence version replaced gi:9256664.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 656404
Center clone name: CIRB-HL_2075C7
-----
Summary Statistics
Consensus quality: 153352 bases at least Q40
Consensus quality: 154674 bases at least Q30
Consensus quality: 154871 bases at least Q20
Estimated insert size: 171000; pulse field gel estimation
Estimated insert size: 154913; sum-of-ctngs estimation
Quality coverage: 9.64 in Q20 bases; pulse field gel estimation
Quality coverage: 10.64 in Q20 bases; sum-of-ctngs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1      6677: contig of 6677 bp in length
*      6678      6777: gap of unknown length
*      6778      155013: contig of 148236 bp in length.
Location/Qualifiers
1. 155013
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CMD-2075C7"
/clone_lib="Caltech human BAC library D"
44427 a 31256 c 31672 g 47558 t 100 others

```

Query Match	59.9%	Score 1201.4	DB 2	Length 155013
Best Local Similarity	99.9%	Prod. No. 2.4e-263		
Matches 1202	Conservative	0	Mismatches 1	Indels 0
Gaps				
QY	803	AGGACTTGGACTTAAAGTCGTGATGACCTTCCCAATCAGATGAGCATGGATGATTTGGCCAGA	862	
Db	99078	AGGACTTGGACTTAAAGTCGTGATGACCTTCCCAATCAGATGAGCATGGATGATTTGGCCAGA	99137	
QY	863	AATGAGAAGAAAGTTTGCAGATGATTTGCAAAAGACAGACAGAGTGGTGTCAAT	922	
Db	99138	AATGAGAAGAAAGTTTGCAGATGATTTGCAAAAGACAGACAGAGTGGTGTCAAT	99197	
QY	923	CTTTGACGGCACAATATGCTGTGTGATCCGGTCTTACTTTTGAGAGAGTTTTCATCA	982	
Db	99198	CTTTGACGGCACAATATGCTGTGTGATCCGGTCTTACTTTTGAGAGAGTTTTCATCA	99257	
QY	983	TGATCACAACAAGSAGAGGGGCTCTGTTATCACAGTGAGAGCAGAGCTGAGCCCGG	1042	
Db	99258	TGATCACAACAAGSAGAGGGGCTCTGTTATCACAGTGAGAGCAGAGCTGAGCCCGG	99317	
QY	1043	CCCTGCACCTCTGCTGTTTAAACCCAGGCATCCCTCTTCCAAAAGGATCCCTTCAT	1102	
Db	99318	CCCTGCACCTCTGCTGTTTAAACCCAGGCATCCCTCTTCCAAAAGGATCCCTTCAT	99377	
QY	1103	AGGAGAACAACACTGAGAGAGTACTTGAAGAATTTGATTCAGCCGGGAAGAGATTTATCA	1162	
Db	99378	AGGAGAACAACACTGAGAGAGTACTTGAAGAATTTGATTCAGCCGGGAAGAGATTTATCA	99437	
QY	1153	GCTTAACGCACATTAATATCATGAAACTAATTAAGTTAAAGTCATAGTCTCAATCCACAG	1222	
Db	99438	GCTTAACGCACATTAATATCATGAAACTAATTAAGTTAAAGTCATAGTCTCAATCCACAG	99497	
QY	1223	CCCAAGGCTCAAGTAAATTTGTAATCTGCATTTACAGTGTAGAGTAACATTAACATTTGT	1282	
Db	99498	CCCAAGGCTCAAGTAAATTTGTAATCTGCATTTACAGTGTAGAGTAACATTAACATTTGT	99557	
QY	1283	ATGCATGGAACAATGAGAGAACATATTACAGTGTCTTACCACCTTAATCAGAAAAGAA	1342	
Db	99558	ATGCATGGAACAATGAGAGAACATATTACAGTGTCTTACCACCTTAATCAGAAAAGAA	99617	
QY	1343	TTACAGACTCGATTTCAACAGTGTGATTAATTTCTAAAATGTTATCATTTAGGCGCTTT	1402	
Db	99618	TTACAGACTCGATTTCAACAGTGTGATTAATTTCTAAAATGTTATCATTTAGGCGCTTT	99677	
QY	1403	TGATTTATTAACCTTTGGGTCCTTAATCTAATAATTATGTAAGTTATTCGCTTCCAGTTT	1462	
Db	99678	TGATTTATTAACCTTTGGGTCCTTAATCTAATAATTATGTAAGTTATTCGCTTCCAGTTT	99737	
QY	1463	GCTTGATTAATTTGTGTGATTTAGATTCCTTGACTTAATTTTGAGTGGGTTCTATGTA	1522	
Db	99738	GCTTGATTAATTTGTGTGATTTAGATTCCTTGACTTAATTTTGAGTGGGTTCTATGTA	99797	
QY	1523	AAAGAAATGATATTTCTGTGAAGACATCGATTAACATTTTATTAACCTCTTGATTTTACA	1582	
Db	99798	AAAGAAATGATATTTCTGTGAAGACATCGATTAACATTTTATTAACCTCTTGATTTTACA	99857	
QY	1583	ATGTAGAAAATGAGAGAAATGCCCAAAATTTATGTGTGATTAAGTACGCTGAAACAGACT	1642	
Db	99858	ATGTAGAAAATGAGAGAAATGCCCAAAATTTATGTGTGATTAAGTACGCTGAAACAGACT	99917	
QY	1643	GATTGTGTGATTCAGAGCCCTTTTGTCTGTGTGTTCAATGATCCCTTAAGCACAATGCA	1702	
Db	99918	GATTGTGTGATTCAGAGCCCTTTTGTCTGTGTGTTCAATGATCCCTTAAGCACAATGCA	99977	
QY	1703	AACTTTAGCAACAGTATACACACTTTGTAATTTGCAAGAAAAGTTTACCTGTATTTGAA	1762	
Db	99978	AACTTTAGCAACAGTATACACACTTTGTAATTTGCAAGAAAAGTTTACCTGTATTTGAA	100037	
QY	1763	TCAGAAATGCTTCAACAGGAAAACAAATATCCAAAATTAAGAGAGAAATGTTGGGCTCAC	1822	
Db	100038	TCAGAAATGCTTCAACAGGAAAACAAATATATCCAAAATTAAGAGAGAAATGTTGGGCTCAC	100097	

QY	1823	TACGTAGAGTCCACAGGAGGAGACAGATTATTTAGGGTTCCCGTATCCAGTAACCTGGGGCC	1882
Db	100098	TACGTAGAGTCCACAGGAGGAGACAGATTATTTAGGGTTCCCGTATCCAGTAACCTGGGGCC	100157
QY	1883	TGTTTTCCCGTGGGCTCTGAGGCTGCACAGCTTTCCTTCCATGCTGTATTTCTCT	1942
Db	100158	TGTTTTCCCGTGGGCTCTGAGGCTGCACAGCTTTCCTTCCATGCTGTATTTCTCT	100217
QY	1943	CAGCGGTGTACCAAGTTCTTGATCTTTATACCACACACAGCAACATCCAGAAATTAAGT	2002
Db	100218	CAGCGGTGTACCAAGTTCTTGATCTTTATACCACACACAGCAACATCCAGAAATTAAGT	100277
QY	2003	TCTT 2005	
Db	100278	TCTT 100280	
RESULT 13			
LOCUS	AX401900	1504 bp	DNA
DEFINITION	Sequence 1576 from Patent WO0210453.		
ACCESSION	AX401900		
VERSION	AX401900.1	GI:21338080	
KEYWORDS			
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
AUTHORS	1. Mendrick, D., Porter, M.W., Johnson, K.R., Castle, A.L. and Elashoff, M.R.		
TITLE	Molecular toxicology modeling		
JOURNAL	Patent: WO 0210453-A 1576 07-FEB-2002;		
FEATURES	Gene Logic, Inc. (US)		
source	1. 1504 Location/Qualifiers		
BASE COUNT	375 a 367 c 408 g 354 t		
ORIGIN			
Query Match	41.4%; Score 830; DB 6; Length 1504;		
Best Local Similarity	76.3%; Pred. No. 5.5e-179;		
Matches 10/3;	Conservative 0; Mismatches 325; Indels 8; Gaps 4;		
QY	72	CTGCAGAGGCATCTCGTCTGTGAGCTGTCCGACCTCGGCCGCCGCTTCTGTGCTATG	131
Db	2	CTGCAGAGGCATCTCGTCTGTGAGCTGTCCGACCTCGGCCGCCGCTTCTGTGCTATG	61
QY	132	GTCCTGCTGACTTCCGGGCGCGCTGTGTAGCGCTGGACCGGCGCCGGCTCCGCTAGAC	191
Db	62	ATCTGCGCGGACTTCCGGGCGCGCGGTGTGCTGTGGAACAGATGGGCTCGTGAACAC	121
QY	192	GATGACCCGTTGGGCGCGGCGCAAGCGCTGCGTAGTGTGAGACTTGACAGACCGCGGGA	251
Db	122	CCAGTCACTGTGGCCCGAGGCAAGCGCTGCGTGGGCGCTGGAAGGCGTCTCGGGA	181
QY	252	GCGCGCGTGTGGGCGCGCTGTGTGCAAGCGGTCGATGTGTGTGAGCGCTTCCGCGCG	311
Db	182	GCGCGCGTGTGGGCGCGCTGTGTGCAAGCGGTCGATGTGTGTGAGCGCTTCCGCGCG	241
QY	312	GGTGTGATGGAAGAACTCCACGCTGGGCGCCAGAGATTTCTGACGCGGGAATTCAGAGCTT	371
Db	242	GGTGTGATGGAAGAACTCCACGCTGGGCGCGAGACTCTACGCGAGCAATCCAAAGCTC	301
QY	372	ATTATTCAGGCTGAGTGGATTTGGCCACAGTCAGAGAAAGCTTCTGCGGTTTACCTGGCAC	431
Db	302	ATTATTCAGGCTGAGTGGATTTGGCCACAGTCAGAGAAATTTTCTCCAAAGTACCTGGCCAT	361
QY	432	GATATCAACTATTTGGCTTGTGACGCTGTTCTCTCAAAAATTTGGCAGAACTGTGAGAAAT	491

D	362	GACATCAACTATGTGGCTTTGTACAGTGTCTCTGTCCATCAAGATTTGGCAGGAGGCGGTGAAAC	421
O	492	CCGATGCCCCCGATGATCTCCGTGGCTACTCTTCTGTGGTGGGCGCTTATCTGTGCACTG	551
D	422	CCATACCCCTCCCTGAAACCTCCCTGGCCCACTTTTGTGGCGGTGGCCCTATGTGCATTTG	481
O	552	GGATTTAATAATGGTCTTTTGTGACGCAACAGCACTGGCAAGGGTCAGGTGATTTGATGCA	611
D	482	GGATTTTGTGGCTCTCTTCGAAAGCAGCGGGCTGTGGCTTAGGGCAGGTGATTTGATGG	541
O	612	AATATGTGGAGGAACACAGATTTTAACTCTTTCTGTGGAAACCTCAGAAATGAGAT	671
D	542	ACATGTGTGGAGGAACAGCATCTTAACTACTTCTGTGGAAACCTCAGCCATGGAT	601
O	672	CTGTGGAGGACACTCGAGGACAAACATGTTGGATGTGTGGAGCACCTTTCTATAGACT	731
D	602	CTGTGGGACACAGCTTCGAGGGCAAAACCTGTTAATATGGCGGGCACCTTCTTACACAAAC	661
O	732	TACAGACACGAGATGGGGGAAATTCATGCTCTTGTGGACAAATAGAACCCCACTTACAG	791
D	662	TAAAGACCGGAGATGGGGAGTTCAATGCTCTATAGTTCAAATAGAACCCCACTTACAC	721
O	792	CTGTGTATCAAGGACTTGGACTTAAAGTGTGATGAACCTTCCCATCAGATGAGCATGAT	851
D	722	CTGTGTCTTAAAGGACTTGGACTTGAAGTGTGATGAGAACCTTCCCAAGCATGAGATGAA	781
O	852	GATTTGGCCAGAAATGAGAAGAGTTTCCAGATTTATTTGCCAAGAGACCAAGCCAGAG	911
D	782	GATTTGGCCAGAAATGAGAAGAAATTTCCAGATGTGTTTCCAAAGAAACATAGAGCCAG	841
O	912	TGATGTCAAACTTTTGACGGCACAGATCTCGTGTGACTCCGGTCTTCACTTTGAGAG	971
D	842	TGATGTCAAACTTTTGACGGGCAAGATCATGTGTGACCCCATGCTGACTTGAAGAG	901
O	972	GTGTGTCAATCATGTATCAACAAGAGAGGGGGCTCGTTTATCCAGAGTAGAGACAGAC	1031
D	902	GGCTTCACACACAGCACACAGAGAGGGGGCTCTTATCATGATGATGAGGACCAT	961
O	1032	GTGAGCCCCCGCTCGACCTCGCTGTAAACACCCACCATCCCTTCTTCAAAAG	1091
D	962	GCATGGCCCCCTGTGACCCCAAGCTTTCAGAAACCCCTCTCTTCTTGTGCCAAAG	1021
O	1092	GATCTTTTCATAGAGAACACACTGAGAGATACTTGAAGATTTTGGATTGACGCCGAA	1151
D	1022	GACCTCTCTGTGGAGAGCACACACTGTAAGAGTGGTTTAAACACTATGAGTATGACAGAA	1081
O	1152	GAGATTTTACGCTTAACTCAGATTAATAATCTTGAAGATTAATAGGTAAGATGCTC	1211
D	1082	GAGATCTCATGCTGCACCTCGGTATGAATCTTTGAAAGTAAATAGCTTAAAGCCACACCT	1141
O	1212	TAACTTCCAGCCCCACGGCTCAAGAGATTTTGAATPACTGTGATTTACAGTGTAGTAAC	1271
D	1142	TGACT--CAGSTTACACAGCTCAAGTGAATCTGAGAGCTGTATGTACTGAGAGAGATG	1199
O	1272	CATTAACATTTGATCATGAGAAACATGAGAGAAAGTATTTCATGCTCCACACCTTAAT	1331
D	1200	CCACACACTGTCTGATATGAAATGTGAATGAACGTAATGAAGTAAATCCAAATATTCCAA	1259
O	1332	CAGAAAGAAATTTACACATCGATTTTACAGATGATGATGATGATGATGATGATGATG	1391
D	1260	TCAAGACACACAGAAABA--CTGATTTACAGAAATATGACGTGCTCTCACACTGCTATG	1317
O	1392	---ATTAGGCTTTGATTTATTAATAACTTTGGGATCTTATACAAATATATGCTGATAT	1448
D	1318	CGAGCCTCTGATATGAGAGATATTTTGTGTGTGTACTGATATTAACCTGTGGCAGTT--TT	1376
O	1449	CTGCTTCCAGTTTGTCTGATATAT	1474
D	1377	CTGCTTTCACCTTACTTGTGTGAAAT	1402

	LOCUS	RN89905	1504 bp	mRNA	linear	ROD 07-OCT-1997
	DEFINITION	Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.				
	ACCESSION	U89905				
	VERSION	U89905.1				
	KEYWORDS	GI:2145183				
	SOURCE	Rattus norvegicus.				
	ORGANISM	Rattus norvegicus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	REFERENCE	1 (bases 1 to 1504) Schmitz,W., Fingerhut,R. and Conzelmann,E. Purification and properties of an alpha-methylacyl-CoA racemase from rat liver				
JOURNAL	MEDLINE	Eur J Biochem. 222 (2), 313-323 (1994)				
PUBLISHED		94291625				
AUTHORS	TITLE	2 (bases 1 to 1504) Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E. Molecular cloning of cDNA species for rat and mouse liver alpha-methylacyl-CoA racemases				
JOURNAL	MEDLINE	Biochem. J. 326 (Pt 3), 883-889 (1997)				
PUBLISHED		97439733				
AUTHORS	TITLE	3 (bases 1 to 1504) Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E. Direct Submission				
JOURNAL	MEDLINE	Submitted (17-FEB-1997) Physiologic Chemistry II, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany				
FEATURES	source	Location/Qualifiers 1..1504 /organism="Rattus norvegicus" /db_xref="taxon:10116" /tissue_type="liver" 59..1144 /EC_number="5.1.99.4" /function="racemization of 2-methyl-branched fatty acids as CoA esters" /note="required for bile acid synthesis and for catabolism of branched-chain fatty acids" /codon_start=1 /product="alpha-methylacyl-CoA racemase" /protein_id="AA072145.1" /db_xref="GI:2145184"				
CDS		/translation="MTLADFGAEVIVLDRLGCVNPHIANGKRSIALDIKRSPGAV LRRCARADVLEEFRCGVMEKLQDGPTLRDPDKILYRLSFSGSGIFSKVAGHD INVVALSGVLSTIGRSGENPEPLNLADIREFGGGLMCTLGILLAFERTNSGLVID ANNVEATGVASTFETLMKTQAMGLMAOPGNOLDDGAPFYTYKYADEFPNAVGAIEPO FYVTLLKGLGISESELPSOMSIEDMPKKKFADVFARKTKAEWCOJFDGDADCVTPV LTLEEALHGHNRERGSFTIDEEOHACPAPAPQLSTRPAVPASAKRSDSVGHTYEVLK DYGFSOEHIIHLSDRITSESKIKANL."				
BASE COUNT		375 a	367 c	408 g	354 t	
ORIGIN						
Query Match		41.4%; Score 830; DB 10; Length 1504;				
Best Local Similarity		76.3%; Pred. No. 5,56-179;				
Matches 1073;		Conservative 0; Mismatches 325; Indels 8; Gaps 4;				
OY	72	CTCAGAGGCATCTGGTGTGAGACTGTGCCGCGCCCGGCGCGCTTCGTGCTATG	131			
Db	2	CTGCGTGCGCGTAGGGTTCTGTGAGAGCTGTGCAGAGCCGTGCACCAGGCGCTTCGTGCGGGATG	61			
OY	132	GTCCTGCGCTGACTTCGGGGGCGCGCTGTGGTAGCGGTGAGACCGCGCGCTCCCGCATACAC	191			
Db	62	ATCTCGGGGAGACTTCGGGGCGCGAGAGTGTGTCGTGGGACAACACTGGGCTCCGTGTAACCA	121			
OY	192	GTAAGCGCCTTGGGGCGGGGAGAAGCGCTCGCTAGTGCATGAGACCTGAACACCGCGGGGA	251			
Db	122	CCCACTCACCTGGGCCCCGAGGAGCAAGCGCTCGCTGGGGCTGTGACCTGAACGGGCTTC	181			
OY	252	GCCGCGCTGCGCGCGCTGTGCACAAGCGGTCGATTGTGCTGCGAGACCCCTCCGCGCCG	311			
Db	182	GCCGCGGTGTCGGCGCGCATGTGCGACACGCGCGGACGCTGTCCTGTGAGACCCCTTCGCTGC	241			

QY	312	GGTCAATGGAGAAACCTCCAGCGGGGCCAGAACTTCGACGCGGAAAAATCCAGGGCTT	371
Db	242	GGGTCTATGGAGAACTCCAGCTTGGGCCAGAACTCTCCAGGAGACATCCAAAGCTC	301
QY	372	ATTATATCCAGGGCTGAGTGGATTGGCCAGATCCAGAACTTCGTGCGGTTTAACTGGCCAC	431
Db	302	ATCATATCCAGGGCTGAGTGGATTGGCCAGATCCGGAATTTTCTCCAAATGACTGGCCAT	361
QY	432	GATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGTAAGT	491
Db	362	GACATCAACTATATGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGGAGCGGTGAGAAC	421
QY	492	CCGATATGCCCGGATCTCTCGGGGTGACTTTGCTGGGTGGGCGCTTATGTGCTACGTG	551
Db	422	CCATATCCCTCCCTGAAACCTCTCGGCCGATTTTGGTGGGGGCGCTCATGTGCAATTTG	481
QY	552	GGCATTTAATATGGCTCTTTTGTGACCCGACACGCACTGGCGAAGGGTCAAGGTCTATTGATCA	611
Db	482	GGCATTTTGGCGGCTCTCTTGCAGACGACGGGTCTGGCTATGGGAGGATCTATTGATGG	541
QY	612	AATATGGTGGAGAGACAGATATTATAGTCTTTTCTGTGAAAATCTCAGAAATGCACT	671
Db	542	AACATGGTGGAGAGAACGAGATCTTAAGTACTTTCTGTGAAAATCTCAGGACCATGGGT	601
QY	672	CTGAGGGAAGACCTCGAGGACAGAAACATTTGGATGGTGGAGACCTTTATATACGAT	731
Db	602	CTTGGGGCACAGCTCTCAGAGGGCAAAACCTGTATGATGGGGGGCACCTTTCTACACAAAC	661
QY	732	TACAGGACAGCAGATGGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCAGTTTTCACAG	791
Db	662	TACAAGACCGAGATGGGGAGATTCAATGGCTGTATGGTCAATAGAACCCAGTTTTCACACA	721
QY	792	CTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCAAATCATATGACATGAT	851
Db	722	CTGCTGCTTAAAGACTTGGACTTGGATGTGAGAAACCTCCACAGCAGATGAGCATAGAA	781
QY	852	GATTGGCCAGAAATGAATGAAAGTTTGGCAGATGTATTGGCAAAAGAGCAAGGACAGAG	911
Db	782	GATTGGCCAGAAATGAATGAAAGAAATTTGCAAGATGTATTGGCAGAGAGACTTAAGGACAG	841
QY	912	TGCTGTCAAAATCTTTGACGGCACAGATAGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAG	971
Db	842	TGHTGCCAAGATCTTTGACGGGACAGATAGCATGTGTGACCCCAAGTGCTGACTTTGAGGAG	901
QY	972	GTTTGTATCATGTATCAACAACAGGAACGGGGCTGTTTATACACAGTGAAGGACAGAC	1031
Db	902	GCCCCCACACACAGCACAACAGAGAAACGGGGCTCCTTATCATCATGATGAGGACGACAT	961
QY	1032	GTCAGCCCCCGGCTGTGACCTGTGCTTAAACACCCGACGACATCCCTTTCAAAGG	1091
Db	962	GCATATCCCCGCTCTGTGACCCCAAGCTTTCCAGAACCCCTGCTGTCTTCTGCCAAAAGG	1021
QY	1092	GATCCCTTTCATAGAGAAACACACTGAGAGATACTTGAAGAATTTGGATTACGCCGCGAA	1151
Db	1022	GATCCCTTCTGTGGGAAGAGCACTGTATAGAGGTGCTTAAAGACTATAGATTGATCGTAGGA	1081
QY	1152	GAGATTTATAGCTTAACTCAGATTAATAATCATTTGAAGTAAATAGGTAAAGCTATGCTC	1211
Db	1082	GAGATTTCATAGCTGCTGCTGTGATTAATAATCATTTGAAGTAAATAGCTTAAAGCCAACTC	1141
QY	1212	TAACTTCAGAGGCCAGCGCTCAAGTGAATTTGAATATCTGCATTTACAGGTGAGATACAA	1271
Db	1142	TGACTCTCAAGTTTCAACGCTCAAGTAAATCTGAAGCTGTATCTGTACTGGGAAGGATG	1199
QY	1272	CATATACCTTATAGCATGGAATAAGTAGAGAAACAGATTACAGTGTCCATACACACTAT	1331
Db	1200	CCACACACTCTCGTATAGGAATGTAAATAGAACAGTAAATGAAGTATCCAAATATTCCAA	1258
QY	1332	CAGAAGAGATTTACAGACTCTTATCTACAGTATGATTTGAATCTTAAATGGTTTATC	1391
Db	1260	TCAAGACACACAGAAAGACTTATATTCAGAGAAATGACTGTGCTCTACAGCTGCTCATC	1317


```

Db 1205 ATGGAAATGTGAATGACAGTAATGAAGTAATCCAAATATTCCAATCAAGACACAAGAA 1264
Qy 1347 AGACTCTGATTCTACAGTATGATTCCTPAAAAATGGTATC--ATTAGGCTTTT 1403
    ||| ||||| | || |||| | || | ||| | |||
Db 1265 AGA--CTGATTCAGAGAAATGACTGTGCTCTCACACTGCTCATCCGAGCCTTGATGA 1322
Qy 1404 GATTATTAATACTTTGGGTACTTATTAATAATTATGGTAGTATTTCTGCCCTTCAGTTTG 1463
    | ||| | || ||||| || ||| || ||| ||||| ||| ||
Db 1323 GGAGTATTTTGTGTGTACTGATTAATACTGTGGCAGTT-TCTGCCCTTCAGCTTA 1381
Qy 1464 CTTGATATATTT 1474
    |||| | ||
Db 1382 CTTGGTGAAAGT 1392

```

Search completed: April 1, 2003, 22:36:18
 Job time : 6254 secs

us-09-967-305-3.rge

score greater than or equal to the score of the
and is derived by analysis of the total score d

!tuo1soetay : owoH

On 8

Search Time 34.18 Seconds

(without alignments)
9757.708 Million cell updates/sec

...ataaggtaaagctagtctc 1146

residues

Parameters: 4109280

redicted by chance to have a

Result No.	Score	Match	Query Length	DB	ID
1	1146	100.0	2005	9	AF158378
2	1142.8	99.7	1621	6	AX106326
3	1142.8	99.7	1621	6	AX110617
4	1142.8	99.7	1621	6	AX200477
5	1142.8	99.7	1621	6	AX267132
6	1141.2	99.6	1674	9	AK009912
7	1136.4	99.2	2041	9	AF047020
8	1093.4	97.4	2068	9	HSA130733
9	812.4	70.9	2946	9	BC009471
10	776.8	67.8	1504	6	AX401900
11	776.8	67.8	1504	6	RN089505
12	753.8	65.8	1498	10	RN2471C0
13	745.4	65.0	1472	10	BC015825
14	735.2	64.5	1317	9	AK022765
15	735.2	64.2	1515	10	MM089906
16	428.4	37.4	430	6	AX368794
17	409	35.7	90111	9	AC008954
18	409	35.7	131856	2	AC008971
19	409	35.7	155013	2	AC026707
20	406.6	35.5	773	6	AX106222
21	406.6	35.5	773	6	AX140513
22	406.6	35.5	773	6	AX200373
23	406.6	35.5	773	6	AX267029
24	403.2	35.2	793	6	AX106252
25	403.2	35.2	793	6	AX140543
26	403.2	35.2	793	6	AX200403
27	403.2	35.2	793	6	AX267059
28	400.2	34.9	816	6	AX106221
29	400.2	34.9	816	6	AX140512
30	400.2	34.9	816	6	AX200372
31	400.2	34.9	816	6	AX267028
32	316.4	27.6	421	6	AX302796
33	277.8	24.2	140132	2	AC138089
34	263.8	22.0	1360	3	AX121652
35	251.4	21.9	1462	6	E066592
36	244.2	21.3	19275	2	AC019718
37	244.2	21.3	147799	3	AC004759
38	244.2	21.3	156806	3	AC003047
39	244.2	21.3	173422	3	AC007467
40	244.2	21.3	267284	3	AE003668
41	236.4	20.6	5537	6	E06693
42	210.2	18.3	12832	1	AE005858
43	207	18.1	42224	1	MLCB33
44	205	17.1	348450	1	MLEPRT14
45	205	17.1	149553	1	AE006996

AX1140617 Sequence					
AX2200477 Sequence					
AX267132 Sequence					
AK009912 Homo sapi					
AF047020 Homo sapi					
HSA130733 Homo sapi					
BC009471 Homo sapi					
AX401900 Sequence					
U89505 Rattus norv					
Y081472 R. norvegic					
BC015825 Mus musc					
AC022765 Homo sapi					
U89906 Mus muscul					
AX368794 Sequence					
AC008954 Homo sapi					
AC008971 Homo sapi					
AC026707 Homo sapi					
AX106222 Sequence					
AX140513 Sequence					
AX200373 Sequence					
AX267029 Sequence					

ALIGNMENTS

RESULT	1
AF158378	
LOCUS	2005 bp mRNA linear PRI 11-FEB-2000
DEFINITION	Homo sapiens alpha-methylacyl-CoA racemase (RM) mRNA, complete cds.
ACCESSION	AF158378
VERSION	AF158378.1 GI:6653127
KEYWORDS	.
SOURCE ORGANISM	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 2005) Ferdinandusse,S., Denis,S., Clayton,P.T., Graham,A., Rees,J.E., Allen,J.T., McLean,B.N., Brown,A.Y., Vreken,P., Waterham,H.R. and Wanders,R.J.


```

REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu, J., Skelky, Y.A., Reed, S.G., and Cheever, M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 107 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..1621
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN
Query Match 99.7%; Score 1142.8; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 1.6e-248;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGAGGGGATCTCGGTCTGTGAGCTGTCCGGCCCTCGGGCCCGCTTCTGT 60
DB 5 ATGGCACTGAGGGGATCTCGGTCTGTGAGCTGTCCGGCCCTCGGGCCCGCTTCTGT 64
QY 61 GCTATGCTCTGTGCTGACTTGGGGCGCTGTGTGACGCTGAGCCGGCTCCCGC 120
DB 65 GCTATGCTCTGTGCTGACTTGGGGCGCTGTGTGACGCTGAGCCGGCTCCCGC 124
QY 121 TAGACGTGAGCCGCTTGGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCG 180
DB 125 TAGACGTGAGCCGCTTGGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCG 184
QY 181 CGGGAGAGCCGCGTGTGCGGCGTGTGCAAGCGCTGATGCTGTGAGCCCTTC 240
DB 185 CGGGAGAGCCGCGTGTGCGGCGTGTGCAAGCGCTGATGCTGTGAGCCCTTC 244
QY 241 CGCGCGGTGTCATGAGAACTCCAGCTGAGGCGCCAGAGATTGTGAGGGGAAATCA 300
DB 245 CGCGCGGTGTCATGAGAACTCCAGCTGAGGCGCCAGAGATTGTGAGGGGAAATCA 304
QY 301 AGGCTATTATTAAGCAGGCTGAGTGAGATTGGCCAGCAGAGCTTCGCCGTACT 360
DB 305 AGGCTATTATTAAGCAGGCTGAGTGAGATTGGCCAGCAGAGCTTCGCCGTACT 364
QY 361 GGGCAGATATCACTATTGGCTTGTGACGCTTCTCTCAAAATTGGCAAGTGT 420
DB 365 GGGCAGATATCACTATTGGCTTGTGACGCTTCTCTCAAAATTGGCAAGTGT 424
QY 421 GAGAAATCGATATGCCCGCTGAATCTCCTGCTACTTTGCTGTGGCTTATGT 480
DB 425 GAGAAATCGATATGCCCGCTGAATCTCCTGCTACTTTGCTGTGGCTTATGT 484
QY 481 GCACTGGGCAATTAATGCTCTTTTGGACGCGCACAGCACTGGCAAGGTCAGT 540
DB 485 GCACTGGGCAATTAATGCTCTTTTGGACGCGCACAGCACTGGCAAGGTCAGT 544
QY 541 GATGCAAAATATGTTGGAAGAAACAGCATATTAGTCTTTTGTGGAATCAGANA 600
DB 545 GATGCAAAATATGTTGGAAGAAACAGCATATTAGTCTTTTGTGGAATCAGANA 604
QY 601 TCGAGCTGTGGGAAGACACTCGAGAGCAAGCACTGTGATGATGAGACACTTCT 660
DB 605 TCGAGCTGTGGGAAGACACTCGAGAGCAAGCACTGTGATGATGAGACACTTCT 664
QY 661 AGCACTTACAGAGACAGATGGGAATTCATGCTTTGAGACATTAAGACCCAGT 720
DB 665 AGCACTTACAGAGACAGATGGGAATTCATGCTTTGAGACATTAAGACCCAGT 724
QY 721 TAGGAGCTGCTGATCAAAAGCACTTGACATAAGTCTGATGAACTCCCATCAGT 780
DB 725 TAGGAGCTGCTGATCAAAAGCACTTGACATAAGTCTGATGAACTCCCATCAGT 784
QY 781 ATGATGATGGCCAGAAATAGAGAGAGTGTGACATGATATTGGCAAGAGCAGAG 840
DB 785 ATGATGATGGCCAGAAATAGAGAGAGTGTGACATGATATTGGCAAGAGCAGAG 844

QY 841 GCAGAGTGTGTCAAAATCTTTGACGAGCAGATGCTGTGTGACTCCGGCTTGAATTT 900
DB 845 GCAGAGTGTGTCAAAATCTTTGACGAGCAGATGCTGTGTGACTCCGGCTTGAATTT 904
QY 901 GAGAGAGTGTGTATCATGATGATCAACAAGAGAGGGGCTGTATTATCACACTGAGAG 960
DB 905 GAGAGAGTGTGTATCATGATGATCAACAAGAGAGGGGCTGTATTATCACACTGAGAG 964
QY 961 CAGAGAGTGTGAGCCCGGCGCTGACCTGCTGTGTTAAACACCCAGCATCCCTTTTC 1020
DB 965 CAGAGAGTGTGAGCCCGGCGCTGACCTGCTGTGTTAAACACCCAGCATCCCTTTTC 1024
QY 1021 AAAAGAGATCTTCAATAGAGAACACACTGAGAGATCTTGAAGATTGATTCAGC 1080
DB 1025 AAAAGAGATCTTCAATAGAGAACACACTGAGAGATCTTGAAGATTGATTCAGC 1084
QY 1081 CGCGAAGATTTATCAAGCTTAATCAAGATAAATCATTTGAAGTAATTAAGTAAGCT 1140
DB 1085 CGCGAAGATTTATCAAGCTTAATCAAGATAAATCATTTGAAGTAATTAAGTAAGCT 1144
QY 1141 AGTCTC 1146
DB 1145 AGTCTC 1150

RESULT 3
AX140617 1621 bp DNA linear PAT 31-MAY-2001
LOCUS AX140617
DEFINITION Sequence 107 from Patent WO0134802.
ACCESSION AX140617
VERSION AX140617.1 GI:14280735
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
Skelky, Y.A., and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 107 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..1621
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN
Query Match 99.7%; Score 1142.8; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 1.6e-248;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGAGGGGATCTCGGTCTGTGAGCTGTCCGGCCCTCGGGCCCGCTTCTGT 60
DB 5 ATGGCACTGAGGGGATCTCGGTCTGTGAGCTGTCCGGCCCTCGGGCCCGCTTCTGT 64
QY 61 GCTATGCTCTGTGCTGACTTGGGGCGCTGTGTGACGCTGAGCCGGCTCCCGC 120
DB 65 GCTATGCTCTGTGCTGACTTGGGGCGCTGTGTGACGCTGAGCCGGCTCCCGC 124
QY 121 TAGACGTGAGCCGCTTGGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCG 180
DB 125 TAGACGTGAGCCGCTTGGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCG 184
QY 181 CGGGAGAGCCGCGTGTGCGGCGTGTGCAAGCGCTGATGCTGTGAGCCCTTC 240
DB 185 CGGGAGAGCCGCGTGTGCGGCGTGTGCAAGCGCTGATGCTGTGAGCCCTTC 244
QY 241 CGCGCGGTGTCATGAGAACTCCAGCTGAGGCGCCAGAGATTGTGAGGGGAAATCA 300

```

Db 245 CGCGCGGTGTCAATGAGAAAACCTCCAGCTGGGCCACAGATTTCTGCAGCGGGAATTCAC 304
 QY AGGCTTATTTATGCGAGGCTGAGTGATTTGGCCAGTACAGAACTTCTCCGGTTAGCT 360
 Db 305 AGGCTTATTTATGCGAGGCTGAGTGATTTGGCCAGTACAGAACTTCTCCGGTTAGCT 364
 QY 361 GGGCAGCATATCAACTATTTGGCTTTGTCAAGTGTTCTCTCAAAATTTGGCAGAACTGT 420
 Db 365 GGGCAGCATATCAACTATTTGGCTTTGTCAAGTGTTCTCTCAAAATTTGGCAGAACTGT 424
 QY 421 GAGAAATCCGATATGCGCGGTAATCTCTGGCTGACATTTGTGTGGTGGCTTATGTGT 480
 Db 425 GAGAAATCCGATATGCGCGGTAATCTCTGGCTGACATTTGTGTGGTGGCTTATGTGT 484
 QY 481 GCACTGGGCAATTAATATGAGTCTTTTGTACCGCACAGCAGCACTGGCAGAGGTCAAGTCAAT 540
 Db 485 GCACTGGGCAATTAATATGAGTCTTTTGTACCGCACAGCAGCACTGGCAGAGGTCAAGTCAAT 544
 QY 541 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAATACTCAGAAA 600
 Db 545 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAATACTCAGAAA 604
 QY 601 TCGAGTCTGTGGGAAGACCTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 660
 Db 605 TCGAGTCTGTGGGAAGACCTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 664
 QY 661 ACAGATTACAGAGCAGAGATGGGGAATTTCACTGGCTGTTGGAGCAATAGAACCCAGTTTC 720
 Db 665 ACAGATTACAGAGCAGAGATGGGGAATTTCACTGGCTGTTGGAGCAATAGAACCCAGTTTC 724
 QY 721 TACGAGCTGCTGATCAAAAGACCTTGACATAAAGTCTGATGACATTTCCCAATCAGATGAGC 780
 Db 725 TACGAGCTGCTGATCAAAAGACCTTGACATAAAGTCTGATGACATTTCCCAATCAGATGAGC 784
 QY 781 ATGATGATTTGGCCAGAAATGAGAAAGATTTGCAGATGATTTGCAAAAGACGAG 840
 Db 785 ATGATGATTTGGCCAGAAATGAGAAAGATTTGCAGATGATTTGCAAAAGACGAG 844
 QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGACTTTT 900
 Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCAAGATGCTGTGTGACTCCGGTTCTGACTTTT 904
 QY 901 GAGGAGTGTGTCAATGATGATCACAAGAGAGGGCTGTTATTCACAGAGAGAG 960
 Db 905 GAGGAGTGTGTCAATGATGATCACAAGAGAGGGCTGTTATTCACAGAGAGAG 964
 QY 961 CAGGAGCTGAGACCCGCCCTGACACTCTGCTGTTAAACACCCAGCATCCTTCTTTT 1020
 Db 965 CAGGAGCTGAGACCCGCCCTGACACTCTGCTGTTAAACACCCAGCATCCTTCTTTT 1024
 QY 1021 AAAAGGATCTTTCATAGAGAACACACTGAGAGATCTTGAAGATTTGGATTGAGC 1080
 Db 1025 AAAAGGATCTTTCATAGAGAACACACTGAGAGATCTTGAAGATTTGGATTGAGC 1084
 QY 1081 CGGCAAGAGATTTATCAGCTTAATCTCAGATTAATCATTTGAAGTAATAGTAAAGCT 1140
 Db 1085 CGGCAAGAGATTTATCAGCTTAATCTCAGATTAATCATTTGAAGTAATAGTAAAGCT 1144
 QY 1141 AGTCTC 1146
 Db 1145 AGTCTC 1150

RESULT 4
 LOCUS AX200477 1621 bp DNA linear PAT 29-AUG-2001
 DEFINITION Sequence 107 from Patent WO0151633.
 ACCESSION AX200477
 VERSION AX200477.1 GI:15390290
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1621)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
 Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
 TITLE Compositions and methods for the therapy and diagnosis of prostate
 cancer
 JOURNAL Patent: WO 0151633-A 107 19-JUL-2001;
 CORIXA CORPORATION (US)
 FEATURES
 source 1..1621
 location/Qualifiers
 BASE COUNT 461 a 330 c 412 g 418 t
 ORIGIN
 Query Match 99.7%; Score 1142.8; DB 6; Length 1621;
 Best Local Similarity 99.8%; Pred. No 1.6e-248;
 Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCACTGCAAGGCATCTCGTGTGAGCTGCGGCTGGCCCGGCGCTTCTGT 60
 Db 5 ATGCACTGCAAGGCATCTCGTGTGAGCTGCGGCTGGCCCGGCGCTTCTGT 64
 QY 61 GCTATGCTCTGCTGACTTGGGCGCGTGTGTAGCGCTGACCGCGCTCCCGC 120
 Db 65 GCTATGCTCTGCTGACTTGGGCGCGTGTGTGTAGCGCGCGCGCTCCCGC 124
 QY 121 TACGACGTGACCGCTTGGGCGCGGAGCGCTCGCTAGCTGAGCACTGAACAGCG 180
 Db 125 TACGACGTGACCGCTTGGGCGCGGAGCGCTCGCTAGCTGAGCACTGAACAGCG 184
 QY 181 CGGGAGCGCGCGTGTGCGGCGTGTGCAAGCGGTGATGCTGTGAGCCCTTC 240
 Db 185 CGGGAGCGCGCGTGTGCGGCGTGTGCAAGCGGTGATGCTGTGAGCCCTTC 244
 QY 241 CGCGCGGCTGATGAGAAATCTCAGTGGCCCAAGATTTGCAAGCGGGAATTCAC 300
 Db 245 CGCGCGGCTGATGAGAAATCTCAGTGGCCCAAGATTTGCAAGCGGGAATTCAC 304
 QY 301 AGGCTTATTTATGCGAGGCTGAGTGAATTTGGCCAGTACAGAACTTCTGCGGTTAGCT 360
 Db 305 AGGCTTATTTATGCGAGGCTGAGTGAATTTGGCCAGTACAGAACTTCTGCGGTTAGCT 364
 QY 361 GGGCAGCATATCAACTATTTGGCTTTGTCAAGTGTTCTCTCAAAATTTGGCAGAACTGT 420
 Db 365 GGGCAGCATATCAACTATTTGGCTTTGTCAAGTGTTCTCTCAAAATTTGGCAGAACTGT 424
 QY 421 GAGAAATCCGATATGCGCGGTAATCTCTGGCTGACATTTGTGTGGTGGCTTATGTGT 480
 Db 425 GAGAAATCCGATATGCGCGGTAATCTCTGGCTGACATTTGTGTGGTGGCTTATGTGT 484
 QY 481 GCACTGGGCAATTAATATGAGTCTTTTGTACCGCACAGCAGCACTGGCAGAGGTCAAGTCAAT 540
 Db 485 GCACTGGGCAATTAATATGAGTCTTTTGTACCGCACAGCAGCACTGGCAGAGGTCAAGTCAAT 544
 QY 541 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAATACTCAGAAA 600
 Db 545 GATGCAAAATATGTTGGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAATACTCAGAAA 604
 QY 601 TCGAGTCTGTGGGAAGACCTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 660
 Db 605 TCGAGTCTGTGGGAAGACCTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 664
 QY 661 ACAGATTACAGAGCAGAGATGGGGAATTTCACTGGCTGTTGGAGCAATAGAACCCAGTTTC 720
 Db 665 ACAGATTACAGAGCAGAGATGGGGAATTTCACTGGCTGTTGGAGCAATAGAACCCAGTTTC 724
 QY 721 TACGAGCTGCTGATCAAAAGACCTTGACATAAAGTCTGATGACATTTCCCAATCAGATGAGC 780
 Db 725 TACGAGCTGCTGATCAAAAGACCTTGACATAAAGTCTGATGACATTTCCCAATCAGATGAGC 784
 QY 781 ATGATGATTTGGCCAGAAATGAGAAAGATTTGCAGATGATTTGCAAAAGACGAG 840

|||||
Db 785 ATGATATATGGCCAGAAATGAAGAAAGTTGCAGATGATATTGCAAAAGAGAGAGAG 844
OY 841 GCAGAGTGTGTCAAAATCTTTGACGACAGATGCTGTGACTCGGTTGACTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGACAGATGCTGTGACTCGGTTGACTTT 904
OY 901 GAGAGGTGTGTATCATATGATCAAAAGAGAGGCTGTGTATACCAATGAGAG 960
Db 905 GAGAGGTGTGTATCATATGATCAAAAGAGAGGCTGTGTATACCAATGAGAG 964
OY 961 CAGAGGTGTGTATCATATGATCAAAAGAGAGGCTGTGTATACCAATGAGAG 1020
Db 965 CAGAGGTGTGTATCATATGATCAAAAGAGAGGCTGTGTATACCAATGAGAG 1024
OY 1021 AAAAGGATCTTTTATAGAGAGACACAGAGATCTTGAAGATTTGGATTGAC 1080
Db 1025 AAAAGGATCTTTTATAGAGAGACACAGAGATCTTGAAGATTTGGATTGAC 1084
OY 1081 CGGAGAGATTTATAGAGTAACTAGATTAATCATTTGAAGTAAAGTAAAGCT 1140
Db 1085 CGGAGAGATTTATAGAGTAACTAGATTAATCATTTGAAGTAAAGTAAAGCT 1144
OY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 5
AX267133 1621 bp DNA linear PAT 26-OCT-2001
LOCUS AX267133
DEFINITION Sequence 107 from Patent WO0173032.
ACCESSION AX267133
VERSION AX267133.1 GI:16515918
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
AUTHORS Kados, M.D., Fanger, G.R., Heller, M.W., Stolk, J.A., Day, C.H.,
Vedavick, R.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer.
JOURNAL Patent: WO 0173032-A 107 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source 1. 1621
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN
Query Match 99.7%; Score 1142.8; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 1.6e-248;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATGGCACTGAGGAGCATCTCGTCTGAGAGTCTCGGCTCGGCGCCGCGCTTCTGT 60
Db 5 ATGGCACTGAGGAGCATCTCGTCTGAGAGTCTCGGCTCGGCGCCGCGCTTCTGT 64
OY 61 GCTATGCTCTGCTGCTACTTCTGGGGCGGCTGTGTGTAGCCGAGAGCGGCGCTCCGC 120
Db 65 GCTATGCTCTGCTGCTACTTCTGGGGCGGCTGTGTGTAGCCGAGAGCGGCGCTCCGC 124
OY 121 TACGACGTGAGCGGCTTGGGGCGGAGCAAGCGCTGCTAGTGTGACCTGAAGACGCG 180
Db 125 TACGACGTGAGCGGCTTGGGGCGGAGCAAGCGCTGCTAGTGTGACCTGAAGACGCG 184
OY 181 CGGGAGCCGCGCTGCTGGGGCGGCTGTGCAAGCGGTGATGTGCTGTGAGCCCTTC 240
|||||

Db 185 CGGGAGCCGCGCTGCTGGGGCGGCTGTGCAAGCGGTGATGTGCTGTGAGCCCTTC 244
OY 241 CGCGCGGCTGTCAATGAGAAATCTCAGCTGGGCGCAGAGATTTGACAGCGGAAATCCA 300
Db 245 CGCGCGGCTGTCAATGAGAAATCTCAGCTGGGCGCAGAGATTTGACAGCGGAAATCCA 304
OY 301 AGGCTATTTATGCGAGGCTGAGTGTGATTTGGCGACAGAGAACTCTCGCGTTAGCT 360
Db 305 AGGCTATTTATGCGAGGCTGAGTGTGATTTGGCGACAGAGAACTCTCGCGTTAGCT 364
OY 361 GCGCAGATATCAATATTTGGCTTTGTCAGGTGTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 365 GCGCAGATATCAATATTTGGCTTTGTCAGGTGTCTCTCTCTCTCTCTCTCTCTCTCT 424
OY 421 GAGAAATCCGATATGCGCCCGCTGAATCTCTGCTGTGCTGTGCTGTGCTGTGCTGT 480
Db 425 GAGAAATCCGATATGCGCCCGCTGAATCTCTGCTGTGCTGTGCTGTGCTGTGCTGT 484
OY 481 GCAGTGGGCAATTAATATGCTCTTTTGAACGCGACACGCACTGGCAAGGGTCAAGTATT 540
Db 485 GCAGTGGGCAATTAATATGCTCTTTTGAACGCGACACGCACTGGCAAGGGTCAAGTATT 544
OY 541 GATGCAATATGCTGAGAGAGACAGCATATTTAAGTTCTTTTCTGTGAAACTCAGAAA 600
Db 545 GATGCAATATGCTGAGAGAGACAGCATATTTAAGTTCTTTTCTGTGAAACTCAGAAA 604
OY 601 TCGAGTCTGTGGAGAGCACTCTGAGAGCAAGCATGTTGATGGTGGAGCACTTTCTAT 660
Db 605 TCGAGTCTGTGGAGAGCACTCTGAGAGCAAGCATGTTGATGGTGGAGCACTTTCTAT 664
OY 661 ACGACTTACAGAGACAGAGATGAGGAAATTCATGCTGTGTGAGCAATAGAAACCCGATTC 720
Db 665 ACGACTTACAGAGACAGAGATGAGGAAATTCATGCTGTGTGAGCAATAGAAACCCGATTC 724
OY 721 TACGAGTGTGTGATCAAGAGCACTTGAAGTGTGATGAATCTCCCATTCAGATGAGC 780
Db 725 TACGAGTGTGTGATCAAGAGCACTTGAAGTGTGATGAATCTCCCATTCAGATGAGC 784
OY 781 ATGATGATTTGGCCAGAAATGAAGAAAGTTGTCAGATGATTTGCAAGAAAGAGCAAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAAGTTGTCAGATGATTTGCAAGAAAGAGCAAG 844
OY 841 GCAGAGTGTGTCAATCTTTGACGCGACAGATGCTGTGTGACTCGGCTGTGACTTTT 900
Db 845 GCAGAGTGTGTCAATCTTTGACGCGACAGATGCTGTGTGACTCGGCTGTGACTTTT 904
OY 901 GAGAGATTTGTTTCATCATGATACAAACAGAAACGGGCTGTTTATCACAGTGAAGAG 960
Db 905 GAGAGATTTGTTTCATCATGATACAAACAGAAACGGGCTGTTTATCACAGTGAAGAG 964
OY 961 CAGAGCTGAGAGCCCGCCCTGCACTCTGCTGTTAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGAGCTGAGAGCCCGCCCTGCACTCTGCTGTTAACACCCAGCCATCCCTTCTTC 1024
OY 1021 AAAAGGATCTTTTATAGAGAGACACACTGAGAGTATTTGAAGATTTGGATTGAC 1080
Db 1025 AAAAGGATCTTTTATAGAGAGACACACTGAGAGTATTTGAAGATTTGGATTGAC 1084
OY 1081 CGCGAAGATTTATGAGTAACTAGATTAATCATTTGAAGTAAAGTAAAGT 1140
Db 1085 CGCGAAGATTTATGAGTAACTAGATTAATCATTTGAAGTAAAGTAAAGT 1144
OY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 6
AK00912 1674 bp mRNA linear PRI 01-AUG-2002
LOCUS AK00912
DEFINITION Homo sapiens cDNA FLJ10050 f1s, clone HEMBA1001257, highly similar
to Homo sapiens mRNA 2-methylacyl-CoA racemase.
ACCESSION AK00912

VERSION	AK000912.1	GI:7021873
KEYWORDS	oligo capping; fts (full insert sequence);	
SOURCE	Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, cloneLib:HEMBA1 clone:HEMBA1001257.	
ORGANISM	Homo sapiens	
REFERENCE	Enkaiyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nadekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.	
TITLE	NEO human cDNA sequencing project	
JOURNAL	unpublished	
REFERENCE	2 (bases 1 to 1674)	
AUTHORS	Isogai,T. and Otsuki,T.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	
COMMENT	NEO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.	
FEATURES	location/Qualifiers	
source	1..1674	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="HEMBA1001257"	
	/tissue_type="whole embryo, mainly head"	
	/clone_lib="HEMBA1"	
	/dev_stage="embryo, 10 weeks"	
	/note="cloning vector: PMEB8SFL3"	
BASE COUNT	432 a 349 c 451 g 442 t	
ORIGIN		
Query Match	99.6%; Score 1141.2; DB 9; Length 1674;	
Best Local Similarity	99.7%; Pred. No. 3.7e-248;	
Matches 1143; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
OY	1 ATGGCAGTCGACAGGCGATCTCGTCTGTGAGAGCTGTCCGGCTGCGCCCGGCGCCGTTCTGT 60	
Db	82 ATGGCAGTCGACAGGCGATCTCGTCTGTGAGAGCTGTCCGGCTGCGCCCGGCGCCGTTCTGT 141	
OY	61 GCTATGTCCTGCGCTGAGCTTCGGGGCGGGTGTTGGTAAGCGTGGAGCGGCGCGCCGCG 120	
Db	142 GCTATGTCCTGCGCTGAGCTTCGGGGCGGGTGTTGGTAAGCGTGGAGCGGCGCGCCGCGCTCCGC 201	
OY	121 TACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTGCTAGTGCCTTGAGCCTGAAGCAGCG 180	
Db	202 TACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTGCTAGTGCCTTGAGCCTGAAGCAGCG 261	
OY	181 CGGGAGCGCGCTGCTGCGGCTGTGTGTCAGACGCGTGGAGTGTCTGTGGAGCCCTTC 240	
Db	262 CGGGAGCGCGCTGCTGCGGCTGTGTGTCAGACGCGTGGAGTGTCTGTGGAGCCCTTC 321	
OY	241 CGCCCGGCTGTATGGAAGAACTCCAGCTGGGCCAGAGATTCTGCACGCGGAAATATCCA 300	
Db	322 CGCCCGGCTGTATGGAAGAACTCCAGCTGGGCCAGAGATTCTGCACGCGGAAATATCCA 381	
OY	301 AGGCTTATTTATGCCAGCGCTGAGTGGATTGGCCAGTCAGAGAACTTCTGCCGTTAGCT 360	
Db	382 AGGCTTATTTATGCCAGCGCTGAGTGGATTGGCCAGTCAGAGAACTTCTGCCGTTAGCT 441	
OY	361 GGGCCAGATPACATATTGGCTTTGTCCAGGTGTTCCTCAAAAATTGGGAGAGTGGT 420	
Db	442 GGGCCAGATPACATATTGGCTTTGTCCAGGTGTTCCTCAAAAATTGGGAGAGTGGT 501	
OY	421 GAGAAATCCGTAATGCCCGCGCTGAATCTCCTGTGCGTGACTTGTGTGTGTGGGCTTATGTGT 480	

Db	502	GAGATCCGATAGCCCCCGCTGAATTCCTGGCTGACTTTGGTGGTGGGGCTTAATGT	561
Qy	481	GCATGGGCATTATATATGGCTCTTTTGTACCGCACACGCACTGGCAGGGTCAGTATT	540
Db	562	GCACGGGCATTATATATGGCTCTTTTGTACCGCACACGCACTGGCAAGGTCAGTATT	621
Qy	541	GATGCAATATATGGTGGGAAGAACACATATTATTTAACTTTTCTGTGGAAAACTCAGAAA	600
Db	622	GATGCAATATATGGTGGGAAGAACACATATTATTTAACTTTTCTGTGGAAAACTCAGAAA	681
Qy	601	TCGAGCTGTGTGGGAAGAACCTTCGAGACAGAACATGTGTGATGGTGAGCACTTTCTAT	660
Db	682	TCGAGCTGTGTGGGAAGAACCTTCGAGACAGAACATGTGTGATGGTGAGCACTTTCTAT	741
Qy	661	ACGACTTCAGAGACAGCATATGGGATTCATATGGCTGTGTGGGAATGTGAACCCAGATC	720
Db	742	ACGACTTCAGAGACAGCATATGGGATTCATATGGCTGTGTGGGAATGTGAACCCAGATC	801
Qy	721	TACGAGCTGTGTATCAAGAGCACTTCGACTTAAAGTCTGTATGAATCTCCCAATCAGATGAGC	780
Db	802	TACGAGCTGTGTATCAAGAGCACTTCGACTTAAAGTCTGTATGAATCTCCCAATCAGATGAGC	861
Qy	781	ATGATGTATGTGGCCAGAAATGAAAGAAAGTTTGCAGATGTATTGTGCAAAAGACGAG	840
Db	862	ATGATGTATGTGGCCAGAAATGAAAGAAAGTTTGCAGATGTATTGTGCAAAAGACGAG	921
Qy	841	GCAGATGTGTGCAATCTTTGACGGCAGATGCGCTGTGTGACATCCGGTCTGACTTTT	900
Db	922	GCAGATGTGTGCAATCTTTGACGGCAGATGCGCTGTGTGACATCCGGTCTGACTTTT	981
Qy	901	GAGAGGTGTTCATCATATGATACACAAGAGAGCGGGCTCGTTTATCACCAGTGAGAG	960
Db	982	GAGAGGTGTTCATCATATGATACACAAGAGAGCGGGCTCGTTTATCACCAGTGAGAG	1041
Qy	961	CAGGACGTGAGCCCCCGCCCTGACACTCGCTGCTTAAACACCCAGCCATCCCTTCTTC	1020
Db	1042	CAGGACGTGAGCCCCCGCCCTGACACTCGCTGCTTAAACACCCAGCCATCCCTTCTTC	1101
Qy	1021	AAAAGGATTCCTTTCATAGAGAACACACACTGAGAGATACTTGAAGAAATTTGGATTGACG	1080
Db	1102	AAAAGGATTCCTTTCATAGAGAACACACACTGAGAGATACTTGAAGAAATTTGGATTGACG	1161
Qy	1081	CGCGAAGATTTATACACTTAACTCAATATAATCATATTGAAGTAATTAAGCTAAAGCT	1140
Db	1162	CGCGAAGATTTATACACTTAACTCAATATAATCATATTGAAGTAATTAAGCTAAAGCT	1221
Qy	1141	AGTCCTC 1146	
Db	1222	AGTCCTC 1227	
RESULT 7			
LOCUS	AF047020	2041 bp	linear PRI 29-JAN-1999
DEFINITION	Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.		
ACCESSION	AF047020		
VERSION	AF047020.1	GI:4204096	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens.		
REFERENCE			
TITLE	Albers, C., Schmitz, W., and Conzelmann, E.		
JOURNAL	Human alpha-methylacyl-CoA racemase cDNA sequence		
AUTHORS	Albers, C., Schmitz, W., and Conzelmann, E.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-FEB-1998) Biozentrum, University of Wuerzburg, Am		
REFERENCE	3 (bases 1 to 2041)		

AUTHORS Albers, C., Schmitz, W. and Conzelmann, E.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1999) Biozentrum, University of Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
REMARK Sequence update by submitter
COMMENT On Jan 29, 1999 this sequence version replaced gi:2896147.
FEATURES Location/Qualifiers
 1..2041

```

CDS
89. .1237
/EC_number="5.1.99.4"
/function="racemization of 2-methyl-branched fatty acid
CoA esters"
/notes="required for bile acid synthesis and for catabolism
of branched-chain fatty acids"
/codon_start=1
/product="alpha-methylacyl-CoA racemase"
/protein_id="AA010205.1"
/db_xref="GI:4204097"
/translation="MALQGSVMEALSGAPGFCAMVLDPGARVVRNPGSSVDY
SLRGRGRSLVDLQKPGCAAVLRICKRSDULPEPRFGMEKQLQGPITLDRENPRI
IVYRLSGPGSSGSECRAGHDNYLALSLGSLKGRSEBNVAPLNLADPAGGLMKI
ALITIALDLDRTRDKQVLDADWVGTGTVLASSFLKQTSLSMEAPKQNNLQSGAA
PITTTIADGERFMAGALIEPQTELLIKGLGSDLEPSQWSDWPEKKKAFADVAPR
KTKKAEKALFDGDTGCVTVLFFEEVYVHNNKRKSFITSEDSQVSRAPALLNLTMT
PALPSKRPPIGTEHTEVLEEFGRREHREIVQLNSDKRITLIESNRYKAST"
535 a      441 c      527 g      548 t

```

QY	601	TCGAGCTGTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGTGTGAGACACTTTTCTAT	660
Db	689	TCGAGCTGTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGTGTGAGACACTTTTCTAT	748
QY	661	ACGACTTTCAGGACACGAGATGGCGAATTCATGCGCTGTGGACCAATTCAGACCCACATTC	720
Db	749	ACGACTTTCAGGACACGAGATGGCGAATTCATGCGCTGTGTGACCAATTCAGACCCACATTC	808
QY	721	TACGAGCTGTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGTGTGAGACACTTTTCTAT	780
Db	809	TACGAGCTGTGTGGGAAGCACTTCGAGGACAGAAACATGTTGGATGTGTGAGACACTTTTCTAT	868
QY	781	ATGATGATGTGGCCAGAAATGAAGAAGATTGTGCAGATGTATTGTCCAAAGAAGCAAG	840
Db	869	ATGATGATGTGGCCAGAAATGAAGAAGATTGTGCAGATGTATTGTCCAAAGAAGCAAG	928
QY	841	GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCGCTGTGTGATCCGGTTCGTGATTTT	900
Db	929	GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCGCTGTGTGATCCGGTTCGTGATTTT	988
QY	901	GAGAGGTTGTTCATCATGATGATCAACAAGAGAGGGGCTGTTTATCCAGAGTAGAG	960
Db	989	GAGAGGTTGTTCATCATGATGATCAACAAGAGAGGGGCTGTTTATCCAGAGTAGAG	1048
QY	961	CAGGAGCTGAGAGCCCGCCCTCGACCTCGCTGTTTAAACGCCACCATCGCTTTTTC	1020
Db	1049	CAGGAGCTGAGAGCCCGCCCTCGACCTCGCTGTTTAAACGCCACCATCGCTTTTTC	1108
QY	1021	AAAAGGATCTCTTCATAGAGAACACACTGAGGAGATCTTGAAGATTTTGGATTGAC	1080
Db	1109	AAAAGGATCTCTTCATAGAGAACACACTGAGGAGATCTTGAAGATTTTGGATTGAC	1168
QY	1081	CGCGAAGATTTTATCAGCTTAACTCAGATTAATTCATTGAAATTAATTAAGTTAAAGCT	1140
Db	1169	CGCGAAGATTTTATCAGCTTAACTCAGATTAATTCATTGAAATTAATTAAGTTAAAGCT	1228
QY	1141	AGTCTC 1146	
Db	1229	AGTCTC 1234	
RESULT 8	HSAL30733	2068 bp	RNA linear PRI 30-NOV-2001
LOCUS	HSAL30733	Homo sapiens mRNA 2-methylacyl-CoA racemase.	
ACCESSION	U130733	U130733.1 GI:499528	
VERSION	U130733.1	GI:499528	
KEYWORDS	2-methylacyl-CoA racemase.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	Amery, L., Franssen, M., De Nys, K., Mannaerts, G.P. and Van		
JOURNAL	Velthoven, P.P.		
MEDLINE	Mitochondrial and peroxisomal targeting of 2-methylacyl-CoA		
PUBMED	J. Lipid Res. 41 (11), 1752-1759 (2000)		
REFERENCE	2 (bases 1 to 2068)		
AUTHORS	Van Velthoven, P.P.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-JAN-1999) Van Velthoven P.P., Campus Gasthuisberg,		
REMARK	Afdeling Farmacologie, Katholieke Universiteit Leuven, Herestraat,		
FEATURES	B-3000 Leuven, BELGIUM		
source	Location/Qualifiers		
CDS	1..2068		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	89..1237		

```

/codon_start=1
/product="2-methylacyl-CoA racemase"
/protein_id="CAB44062.1"
/db_xref="GI:4995299"
/translation="MALOISYVELSGILPGRXCAMVLAIDFGARVRYRDRPSRKYNS
RIGRKRSLVLDLKOPREPRRAASVDAVCAAGALPDRHGEETPAEPDPAAGKSKAY
LQDAEWIPVQESFCKRAGHDINYLALSGVLSKIGRGNPNYAPALVADFAAGGLMC
ALGIIMALEDRTRDKGVYIDANMEVGTLYLSFLMKTKNSLMEAPLRQNMIDGAP
FYTYRTADGEFMAVGAIEPOYELLIKELGKDELPMQSTIDMDPEKKKFEADYFA
KTKAEMCOIFDGTACVTPVLFEEVHHDKRERSITSEDOVSRLAPLILNT
PAIPSKGDFIPEHREHLEFEFGREREITYOLNSKITEKSKVRSLS"
BASE COUNT      555 a      436 c      528 g      548 t      1 others
ORIGIN
Query Match      95.4%; Score 1093.4; DB 9; Length 2068;
Best Local Similarity 98.2%; Pred. No. 2,6e-237;
Matches 1127; Conservative 0; Mismatches 17; Indels 4; Gaps 2;
QY 1 ATGGCACTGCAGGCACTCTGCTGCTGAGAGCTTCCGGCTGGCCCGGCGCTTCTGT 60
    |||||
DB 89 ATGGCACTGCAGGCACTCTGCTGCTGAGAGCTTCCGGCTGGCCCGGCGCTTCTGT 148
    |||||
QY 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
    |||||
DB 149 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 208
    |||||
QY 121 TACGACGTGAGCGCTTGGGCGCGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
    |||||
DB 209 TACGACGTGAGCGCTTGGGCGCGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 268
    |||||
QY 181 CGGGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
    |||||
DB 269 CGGGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
    |||||
QY 241 CGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    |||||
DB 327 CGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
    |||||
QY 301 AGGCTATTATTATCCAGGCTGAGTGTGATTTGGCCAGT--CAGGAAGCTTTCGCCGGTTAG 358
    |||||
DB 387 AGGCTATTATTATCCAGGCTGAGTGTGATTTGGCCAGTGTGAGGAAGCTTTCGCCGGTTAG 446
    |||||
QY 359 CTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGCTTCTCTCAAAAATTGGCAGAAAGT 418
    |||||
DB 447 CTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGCTTCTCTCAAAAATTGGCAGAAAGT 506
    |||||
QY 419 GTGAGATCGGTATGCGCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
    |||||
DB 507 GTGAGATCGGTATGCGCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
    |||||
QY 479 GTGAGCTGGGCACTTATATGGCTCTTTTGGACCGCACACGACTGGCAGAGGTTCAGGTCA 538
    |||||
DB 567 GTGAGCTGGGCACTTATATGGCTCTTTTGGACCGCACACGACTGGCAGAGGTTCAGGTCA 626
    |||||
QY 539 TTGATGCAAAATATGTTGGAAGACAGCATATTTAAAGTCTTTTCTGTGTGAAAACTCAGA 598
    |||||
DB 627 TTGATGCAAAATATGTTGGAAGACAGCATATTTAAAGTCTTTTCTGTGTGAAAACTCAGA 686
    |||||
QY 599 AATCGAGTCTGTGGGAAGACCTCGAGGACAGAACATGTTGATGGAGGAGCAACCTTTCT 658
    |||||
DB 687 AATCGAGTCTGTGGGAAGACCTCGAGGACAGAACATGTTGATGGAGGAGCAACCTTTCT 746
    |||||
QY 659 ATACGACTTACAGAGACAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGT 718
    |||||
DB 747 ATACGACTTACAGAGACAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGT 806
    |||||
QY 719 TCTACAGCTGCTGATCAAGACACTTGGACTAAAGTCTGTGATGAATCTCCCAATCAGATGA 778
    |||||
DB 807 TCTACAGCTGCTGATCAAGACACTTGGACTAAAGTCTGTGATGAATCTCCCAATCAGATGA 866
    |||||
QY 779 GCATGATATTTGGCAAAATGAGAAAGTTTGCAGATGATTTTGCAAAAGACGA 838
    |||||

```

```

DB 867 GCACGATGATTTGGCCAGAAATAGACAGAGAGTTTGCAGATGATTTTGCAAAAGACGA 926
QY 839 AGGCAAGAGTGTGTCAAATCTTTGACGGGACAGATGCTGTGACCTCCGGTTCTGACTT 898
    |||||
DB 927 AGGCAAGAGTGTGTCAAATCTTTGACGGGACAGATGCTGTGACCTCCGGTTCTGACTT 986
    |||||
QY 899 TTGAGAGGTTGTTTCATCATGATCACAACAGACAGAGGCGCTGTTATTCACGATGAG 958
    |||||
DB 987 TTGAGAGGTTGTTTCATCATGATCACAACAGACAGAGGCGCTGTTATTCACGATGAG 1046
    |||||
QY 959 AGGAGAGCGAGACCCCGGCTGACCTGCTGCTGTTAAACACCCAGCATCCCTTCT 1018
    |||||
DB 1047 AGGAGAGCGAGACCCCGGCTGACCTGCTGCTGTTAAACACCCAGCATCCCTTCT 1106
    |||||
QY 1019 TCAAAAGGATCTTTCATAGAGAGACACACAGTAGAGATCTTGAAGATTTGATTC 1078
    |||||
DB 1107 CCAAGAGGATCTTTCATAGAGAGACACACAGTAGAGATCTTGAAGATTTGATTC 1166
    |||||
QY 1079 GCCGCGAAGATTTATACGCTTAACCTACATTAATCATTTGAAGTAAAGTAAAG 1138
    |||||
DB 1167 GCCGCGAAGATTTATACGCTTAACCTACATTAATCATTTGAAGTAAAGTAAAG 1226
    |||||
QY 1139 CTAGTCTC 1146
    |||||
DB 1227 CTAGTCTC 1234
    |||||

RESULT 9
BC009471      2946 bp      mRNA      linear      PRI 12-JUL-2001
LOCUS      BC009471
DEFINITION      Homo sapiens, Similar to alpha-methylacyl-CoA racemase, clone
ACCESSION      BC009471
VERSION      BC009471.1 GI:14495718
KEYWORDS      MGC.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 2946)
JOURNAL      Direct Submission
SUBMITTER      Submitted (19-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK      NIH-MGC Project URL: http://mgc.ncl.nih.gov
CONTACT      Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Retia Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stolt,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderdyk, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAL Plate: 9 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4204096.
Location/Qualifiers
1..2946
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
source

```



```

Db 182 GCCCGGGTGTGGCGCATGTGGCAGCGCGGACGTTGTCTGGAGCCCTTCCTGTC 241
Oy 247 GGTGTTCATGAGAACTCCAGCTGGCGCCAGAGATTTCTGCAGCGGGAATAATCAAGGCTT 306
Db 242 GGTTCATGTGAGAACTCCAGCTGGCGCCAGAGACTCTACGGCAGGACATCCAAAGCTC 301
Oy 307 ATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCGGCTAGCTGGCCAC 366
Db 302 ATCTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTCCAAAGTGTGGCCAT 361
Oy 367 GATATCAACATTTGGCTTTGTCTGAGTGTCTCTCAAAAATTTGGCAGAGTGGTGAAGAT 426
Db 362 GACATCAACATTTGGCTTTGTCTGAGTGTCTCTCAAAAATTTGGCAGAGTGGTGAAGAC 421
Oy 427 CCGATATCCCGGCTGATTCCTGGTGTGACTTTCTGTGTGGTGGCTTATGTGTGCACTG 486
Db 422 CCATACCTCCCTCCGAACTCTGCGGACCTTTGGTGGCTGGCTTCATGTGCACATG 481
Oy 487 GGCATTAATATGCTCTTTTGGACCGACAGCAGCTGGCAAGGCTCAGGTCATTGATGCA 546
Db 482 GGCATTTTGGCTCTCTCTTCCAGCAGCGGCTGTGGCCTAGGGCAGTTCATTGATGCG 541
Oy 547 AATTATGTTGAGGAGAGATATTTAAGTCTTTCTGTGAGAACTCCAAATTCAGT 606
Db 542 AACATGTTGAGGAGAGAGATATTTAAGTCTTTCTGTGAGAACTCCAAATTCAGT 601
Oy 607 CTGTGGAGACCTCGAGCAGACAGATGTTGGATGGTGGAGCACCCTTCTATAGCACT 666
Db 602 CTGTGGAGACCTCGAGCAGACAGATGTTGGATGGTGGAGCACCCTTCTATAGCACT 661
Oy 667 TACAGGACAGCAGATGGGGAATTCAGTGTGTGGAGCAATAGAACCCAGTCTTACAGAG 726
Db 662 TACAGGACAGCAGATGGGGAATTCAGTGTGTGGAGCAATAGAACCCAGTCTTACACA 721
Oy 727 CTGTGTAAAGAGACTTGGACTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 786
Db 722 CTGTGTAAAGAGACTTGGACTGAAGTCTGATGATGATGATGATGATGATGATGATGAT 781
Oy 787 GATTGGCCAGAAATGAGAGAAAGATTGTCAGATGATGATGATGATGATGATGATGATGAT 846
Db 782 GATTGGCCAGAAATGAGAGAAAGATTGTCAGATGATGATGATGATGATGATGATGATGAT 841
Oy 847 TGTGTCAAAATCTTTGAGCGCAGAGATGCTGTGTGACTCCGCTTGTGACTTTTGAGAG 906
Db 842 TGTGTCAAAATCTTTGAGCGCAGAGATGCTGTGTGACTCCGCTTGTGACTTTTGAGAG 901
Oy 907 GTTGTTCATCATGATCAACAAGAGAGAGGCTGCTTTATCAGCAGTGGAGGAGAGAGAC 966
Db 902 GCCCTCCACACAGCAGCAGACAGAGAGAGGAGGCTCTTCACTGATGAGAGAGAGACAT 961
Oy 967 GTGAGCCCGCCGCTGACCTGTGCTGTAAACACCCCGCCAGTCCCTTTTCAAAAGG 1026
Db 962 GCATGCCCCCGCTGCTGACCCCACTTCCAGAACCCCTGCTTCTTCCCAAAAGG 1021
Oy 1027 GATCTTTCATAGAGAGAACTGAGAGAGATTAAGTGAAGATTTGATTAAGCCGGA 1086
Db 1022 GACCTTCTGTGGAGAGACACTGTGAGAGTGTAAAGCTATGATTAAGTCAAGAGAA 1081
Oy 1087 GAGATTAATCACTTAATCAAGATAAATCAATTAAGTAAAGTAAAGTAAAGTAAAGTAA 1146
Db 1082 GAGATTAATCACTTAATCAAGATAAATCAATTAAGTAAAGTAAAGTAAAGTAAAGTAA 1141

```

```

RESULT 11
LOCUS      RN089905      1504 bp      mRNA      linear      ROD 07-OCT-1997
DEFINITION Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.
ACCESSION  U89905
VERSION     089905.1 GI:2145183
KEYWORDS
SOURCE      Rattus norvegicus.
ORGANISM    Rattus norvegicus.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE 1 (bases 1 to 1504)
AUTHORS  Schmitz,W., Fingerhut,R. and Conzelmann,E.
TITLE     Purification and properties of an alpha-methylacyl-CoA racemase
          from rat liver
JOURNAL   Eur. J. Biochem. 222 (2), 313-323 (1994)
MEDLINE   94291625
PUBMED    8020470
REFERENCE 2 (bases 1 to 1504)
AUTHORS  Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E.
TITLE     Molecular cloning of cDNA species for rat and mouse liver
          alpha-methylacyl-CoA racemases
JOURNAL   Biochem. J. 326 (Pt 3), 883-889 (1997)
MEDLINE   97439733
PUBMED    9307041
REFERENCE 3 (bases 1 to 1504)
AUTHORS  Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E.
TITLE     Direct Submission
          Submitted (17-FEB-1997) Physiological Chemistry II, Biozentrum, Am
          Hubland, Wuerzburg D-97074, Germany
FEATURES  location/Qualifiers
           source
           1..1504
           /organism="Rattus norvegicus"
           /db_xref="taxon:10116"
           /tissue_type="liver"
           59..1144
           /EC_number="5.1.99.4"
           /function="racemization of 2-methyl-branched fatty acids
           as CoA esters"
           /note="required for bile acid synthesis and for catabolism
           of branched-chain fatty acids"
           /codon_start=1
           /product="alpha-methylacyl-CoA racemase"
           /protein_id="AAB72145.1"
           /db_xref="GI:2145184"
           /translation="MILADGAVVIVLDRLGSVNPRLARGRSLALDKRSPGAV
           LRRKARADVLEPFRGVMKILQLEPILRQNPILYARLSGFRSGSGLVYAGHD
           INVALSVGLSTIGRGENEYPPILNLAIDFGGGGLCTGLILALERRSGIGVYD
           ANNVEGTALSTFLMKTOAMGLMAOGRGQNLIDGGAPEYTGITADGEMAVGAIIPQ
           FYLLKGLGLESEELPSQMSIEDMEEMKKFADVARKTKAMCOIFGSTDACVTPV
           LTLEALHHOHNREGSFITDEDOHAKPRAPQLSRTPAVPSAKRDPVSVEHTEVLK
           DYFSOEIHHLSDRILIESNKKANL"
BASE COUNT 375 a 367 c 408 g 354 t
ORIGIN
Query Match 67.8%; Score 776.8; DB 10; Length 1504;
Best local Similarity 80.1%; Pred. No. 1,5e-165;
Matches 913; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

```



```

Db 547 AGGCACTAATTAAGTACTTCTCTGTGAAACTAGGCCATGGGCTGTGGGACAGCCT 606
Qy 622 CGAGGACAGAACATGTGGATGTGGAGCACCCTTCTATACACTTACAGACAGACAT 681
Db 607 CGAGGGCAAAACCTTATGATGGGGGACCTTCTACACACCTACACAGCCGACAT 666
Qy 682 GGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTCTACGAGCTGCTATCAAGA 741
Db 667 GGGGAGTTCATGCTGTGGAGCAATAGAACCCAGTTCTACACACCTTCTTAAAGA 726
Qy 742 CTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 801
Db 727 CTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
Qy 802 AAGAAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
Db 787 AAGAAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
Qy 862 GAGGACACAGTGCCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 921
Db 847 GAGGACACAGTGCCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 906
Qy 922 CACAACAAGAGAGGGGCTGTTATACACAGTGAAGAGAGAGAGAGAGAGAGAGAG 981
Db 907 CACAACAAGAGAGGGGCTGTTATACACAGTGAAGAGAGAGAGAGAGAGAGAGAG 966
Qy 982 GCACCTGCTGTTAAACACCCACCAATCCCTTCTTCAAAAGAGAGAGAGAGAGAG 1041
Db 967 TCACCCAGCTTTCAGAACCCCTTCTGTCCTTCTTCCAAAGAGAGAGAGAGAGAG 1026
Qy 1042 GAACACAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
Db 1027 GAGACACAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
Qy 1102 AACTCAGATTAATCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1146
Db 1087 CACTCGATTAATCATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1131

RESULT 13
BC015825 1472 bp mRNA linear ROD 07-AUG-2002
LOCUS Mus musculus, alpha-methylacyl-CoA racemase, clone MGC:13903
DEFINITION IMAGE:3980103, mRNA, complete cds.
ACCESSION BC015825
VERSION BC015825.1 GI:16198362
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1472)
Strausberg, R.
Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics RefSeq, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gqaps-ref@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Bin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov

```

```

FEATURES
Source
Series: IRAP Plate: 18 Row: C Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6678765.
Location/Qualifiers
1..1472
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
/clone="MGC:13903 IMAGE:3980103"
/tissue-type="Mammary tumor, Metallothionien-TGF alpha
model, 10 month old virgin mouse. Taken by biopsy."
/clone_1lb="NCI_CGAP_Mam1"
/lab_host="DHI08"
/note="Vector: pCMV-Sport6"
46..1128
CDS
/codon_start=1
/product="alpha-methylacyl-CoA racemase"
/protein_id="AAH15825.1"
/db_xref="GI:16198363"
/db_xref="LocusID:17117"
/translation="MYLADGAEVRYNRLSGTGFENFLAKRSLALDLKRSQGVTVL
RRMCARADVLEPFRGVMKELQLEPTELQDPRKLIYALSGFGSGIJSKYAGDHI
NYLALSGVLSKIGRSGENPYPLNLADFGGGLMCTGLIVLALPFRTRSGROIDS
SMVEGTAIVSSFLMKTQPMGLMKOPRGONILDGGAPFTYTKTADGEPMAVGALEPOF
YALLKGLGLESELEPSQMSADMPPEKKFADYPAKKTAEBCOIFDCTDAPVPL
TFEALHGHNRERASFITDEQLPSRPAPLISRTPAVPSAKRDPVGEHTVELRE
YGRFOEILQLHSDRIVESDKLANL"
BASE COUNT 368 a 371 c 396 g 337 t
ORIGIN
Query Match 65.0%; Score 745.4; DB 10; Length 1472;
Best Local Similarity 79.6%; Pred. No. 1,9e-158;
Matches 894; Conservative 0; Mismatches 226; Indels 3; Gaps 1;
Qy 24 CGTGAGCTGCCCGCTGAGCGCCGCGGCGCTGTGCTGATGCTGCTGCTGCTGCTGCG 83
Db 6 CGTCGGGTGCGAGCGCTGCGCGCGCGCGCGCTGTGCGATGCTGCTGCGGACTTCGG 65
Qy 84 GGGCGGTGTGTGACGCGTGGAGCGCGCGCGCGCTGCGCTGAGCGTGAACGCGTTGGCG 143
Db 66 CGCGAGGTGTGTGCGTGAACCGCGCGTGGCGTCC---ACGGGCGAGAAATTTCTGGCG 122
Qy 144 GGGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 203
Db 123 AGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
Qy 204 TCTGTGCAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
Db 183 CATGTGCGACAGCGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
Qy 264 CCAGCTGGGCCAGAGATTCGACGGGGAATTCAGAGCTTATTTATGCGAGGCTGAG 323
Db 243 CCAGCTGGGCCAGAGACTCTACGACGACAAATCCAAAGCTCATCTATGACAGGCTG 302
Qy 324 TGGATTTGGCCAGTCAGGAAGCTTCCGCTTACGTGCGCCACGATATCAACTATTTGGC 383
Db 303 CGGATTTGGCCAAATCGGGAATTTCTCCAAAGTAGCTGGCCATGACATCAATTTGGC 362
Qy 384 TTTGTCAGAGTCTCTCAAAAATTTGCGAGAGGTGAGAGATCCATATGCGCGCTGAA 443
Db 363 TTTATCAGGGCTTGTTCAAAAGATTGCGACAGAGGGGTGAGAACCCCTTACCACCGCT 422
Qy 444 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
Db 423 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
Qy 504 TTTTGACCGCAGACGCTGCGCAAGGCTCAGTCATTTGATGCAATATGTTGGAAGAAC 563
Db 483 CTTTGAACGCAACAGCTGCTGCGCAGGCGAGTCATGATTTCAAGCATGTGGGGAAGGAC 542
Qy 564 AGCATATTAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
Db 543 TGCACTATTAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602

```

Oy	624	AGACAGAAACATGTGGATGGTGGACACCTTTCAATACAGACTTAAGACAGCAGCAGTGG	683
Db	603	AGGACAAAACATCTTAATGATGGCGGTGACACTTTTCACCAACCTTACAAAGCGGAGAGGG	662
Oy	684	GGAATTCATGGCTGTGGAGCATTTAGAACCCAGATTCAGAGAGCTCTGATCAAAAGACT	743
Db	663	GGAGTTCAATGGCTGATGGTGCATTAACAACCCAGTCTGATGACCTCTCTCTTAAAGACT	722
Oy	744	TGAGCAATAAAGCTGATGAATCTCCCAATCAGTAGAGATGGATGATTTGGCCGAATTAAG	803
Db	723	TGAGCTCAGATCTGAGAACTCCCTCCCAATAGCTCAGCAGATTTGGCCGAGATTAAG	782
Oy	804	GAGAAATTTGCAATGTATTTTGCAAAGAAAGCAAGAGCAAGTGGTGTCAATCTTTGA	863
Db	783	GAGAAATTTGCAATGTGTTCACAAAGAAAGCAATAGCAGAAATGGTGCAGATCTTTGA	842
Oy	864	CGGCACATGCGCTGTGACTCGGGTTCGACTTTTGAGAGAGTGGTTCATCATGATCA	923
Db	843	CGGAGACATGCGCTGTGTGACCCCACTGTGACCTTTTGAGAGAGGCCCTCCACACACAGCA	902
Oy	924	CAACAGAAAGAGGGGCTCTTTATCACCAAGTAGAGAGCAGACGTAGGCCCGCCGCTGC	983
Db	903	CAACAGAAAGAGGGGCTCTTCTATCACTGATGAGGAGAGACTCCGAGGCCCGCCGCTGC	962
Oy	984	ACCTTCTGCTTTAAACCAACCCAGCCATCCCTCTTTCAAAAGGATCCTTTTCATAGAGAGA	1043
Db	963	ACCTTCTGCTTCCAAACTCTCTCGCTCCCATCTGCCCCAAAAGGAGACCTCTTGTAGGGAGA	1022
Oy	1044	ACACACTGAGAGATTACTTGAGAGAAATTTTGATTGATTCAGGCCGGAAGAGATTTATCACTTAA	1103
Db	1023	GCACACCGCTAGAAAGTGGTTAGAAAGATGATGATTCAGTGTACGAAGAAATCTTTCACAGTGA	1082
Oy	1104	CTCAGATTAATAATCATTTAGAAAGTAATTAAGGTAAAGCTATGCTC	1146
Db	1083	CTCAGATTAATAATCGTTAGAAAGTATTAAGGTAAAGCCAAATCTC	1125

RESULT	14
LOCUS	AK022765
DEFINITION	AK022765 1317 bp mRNA linear PRI 01-AUG-2002
ACCESSION	Homo sapiens cDNA FLJ12703 f1s, clone NT2RP1000834, highly similar to Homo sapiens alpha-methylacyl-CoA racemase mRNA.
VERSION	AK022765
KEYWORDS	AK022765..1 GI:10434360
SOURCE	Oligo capping: f1s (full insert sequence). Homo sapiens tetracortcinoma cell line:NT2 CDNA to mRNA, clone.lib:NT2RP1 clone:NT2RP1000834. Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1
REFERENCE	
AUTHORS	Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Ofunuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugiyo,S., Shirasaka,H., Sudo,H., Wagatsuma,M., Hosokiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawaji,I., Salvo,K., Yamamoto,J., Wakematsu,A., Nakamura,Y., Nageharu,K., Maehiro,I., Nimomiya,K. and Iwayanagi,T. NEO human cDNA sequencing project Unpublished 2 (bases 1 to 1317) Isogai,T. and Otsuki,T. Direct Submission Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1332-3 Yana, Kisarazu, Chiba 297-0812, Japan (E-mail:genomel@r1.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
JOURNAL	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry for Biotechnology; CDNA full insert sequencing; Research Association for Biotechnology; CDNA library construction, 5'-& 3'-end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
COMMENT	

[illegible]

MU89906 1515 bp mRNA linear ROD 07-OCT-1997
 LOCUS MU89906
 DEFINITION Mus musculus alpha-methylacyl-CoA racemase mRNA, complete cds.
 ACCESSION U89906
 VERSION U89906.1 GI:2145185
 KEYWORDS
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1515)
 AUTHORS Schmitz W., Helander H.M., Hiltunen J.K. and Conzelmann E.
 TITLE Molecular cloning of cDNA species for rat and mouse liver
 JOURNAL Biochem. J. 326 (Pt 3), 883-889 (1997)
 MEDLINE 97439733
 PUBMED 9307041
 REFERENCE 2 (bases 1 to 1515)
 AUTHORS Schmitz W., Helander H.M., Hiltunen J.K. and Conzelmann E.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1997) Physiologic Chemistry II, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany
 FEATURES
 source location/Qualifiers
 1. 1515
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /tissue_type="liver"
 26. 1108
 /EC_number="5.1.99.4"
 /function="racemization of 2-methyl-branched fatty acids as CoA esters"
 /note="required for bile acid synthesis and for catabolism of branched-chain fatty acids"
 /codon_start=1
 /product="alpha-methylacyl-CoA racemase"
 /protein_id="AAB72146.1"
 /db_xref="GI:2145186"
 /translation="MYLADFGAEVVRNRLGSGENFLARGRSLDLKRSQGVTVL RHCARADVLEFFRCGVMEKLLQDPKLIYARLSFGSGSGLFSKVAHDI NYLALSGVLSKIGRSGENPYPLNLADFGGGLMCTGLIVLAFPTSGRQIIDS SMVEGVAVLSFIMKTQPMGLMOPRGONILDGGAFFTYTKADDFPVAVGAIEPOF VALLKGLGLESELPSSOMSSADPMPEMKKFDVFAKKTAKEMCOIFDGTDCVTVPL TPEEAHHHNRERASFPTDGDQLPSPRAPPLISKRPANVPAKRPDSVGEHYEVLE YGFSQEEILQLHSDRIVESDKLANL"
 CDS
 370 c 387 g 346 t
 BASE COUNT 412 a 370 c 387 g 346 t
 ORIGIN
 Query Match 64.2%; Score 735.2; DB 10; Length 1515;
 Best Local Similarity 79.6%; Pred. NO. 4e-156;
 Matches 882; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

Db 298 GCGAATTTTCTCCAAAGTACTGGCCATGATCATCACTATTGGCTTTATCAGCGCTCT
 Qy 399 CTCAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCGTAATCTCTGGCTGACTT
 Db 358 GTCAAAGATTGGCAGAGCGGTGAGAAACCCCTACCCACCGCTCAATCTCTGGCTGACTT
 Qy 459 TGGTGTGGTGGCTTATGTGTGATGCTGAGCGGCAATTAATGGCTTTTATACCGGCACG
 Db 418 TGGCGGTGAGAGGCTCATGTGACACAGTGGGATGTGCTCTCTTATACGACACG
 Qy 519 CACTGGCAGGTCAGGTCTATTAATGCAATATGTGTGAGAAACACATATTAAATGTC
 Db 478 CTCTGGCCGAGGCGAGATCATGATTCAAGCATGTGTGAGAAAGGAGCTCATTAAGTTC
 Qy 579 TTTCTGTGAAAACTCAGAAATCGAGTGTGTGGGAAGCCTCGAGACAGAAATGTT
 Db 538 TTTCTGTGAAAACTCAGAAATCGAGTGTGTGGGAAGCCTCGAGACAGAAATGTT
 Qy 639 GGATGTGAGACACTTTCTATAGACTTACAGACAGCAGATGGGAATTCATGGCTGT
 Db 598 AGATGGGCGTGCACCTTCTACACAACTTACAAAGCAGAGGAGGAGTTGATGCTGT
 Qy 699 TGGAGCAATAGAACCCAGTTCTACAGAGTGTGATCAAGAGACTTGAAGTGA
 Db 658 AGGTCATAGAACCCAGTTCTATGACACTGTGCTTAAAGACTTGCAGTCTGA
 Qy 759 TGAACCTTCCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 Db 718 GGAACCTTCCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 Qy 819 TGTATTGCAAAAGAGCAAG
 Db 778 TGTATTGCAAAAG
 Qy 879 TGTACTCCGCTTCTGACTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 Db 838 TGTACTCCGCTTCTGACTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 Qy 939 CTCGTTATCAGCAGTGAAG
 Db 898 CTCCTTATCAGTATGAG
 Qy 999 CACCCAGCATCCTCTTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 Db 958 AACTCCTCGCTTCTTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 Qy 1059 ACTTGAAGATTGATTCAGCCGCGAAGAGAGATTATCAGCTTAATCAGATTAATCAT
 Db 1018 GCTTAGAGATTATGATTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT
 Qy 1119 TGAAGTAATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGT
 Db 1078 TGAAGTAATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGT

Search completed: April 1, 2003, 22:36:22
 Job time : 3422 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 19:42:24 ; Search time 1952.31 seconds
(without alignments)
9506.702 Million cell updates/sec

Title: US-09-967-305-3

Sequence: 1 atgagcactgcggagcctc.....ataagtaaaagcagctc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estha:*
2: em_estha:*
3: em_estha:*
4: em_estha:*
5: em_estha:*
6: em_estha:*
7: em_estha:*
8: em_estha:*
9: gb_est1:*
10: gb_est1:*
11: gb_est1:*
12: gb_est1:*
13: gb_est1:*
14: gb_est1:*
15: em_estha:*
16: em_estha:*
17: gb_est1:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_hum:*
21: em_gss_hum:*
22: em_gss_hum:*
23: em_gss_hum:*
24: em_gss_hum:*
25: em_gss_hum:*
26: em_gss_hum:*
27: em_gss_hum:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	ID	Description
1	909.2	79.3	968 9	AL558928
2	850.4	74.2	955 12	BG741165
3	812.8	70.9	842 9	AL551698
4	796.4	69.5	824 9	AL545355
5	795.2	69.4	873 9	AL555978
6	787.2	68.7	888 9	AL558977

7	760.4	66.4	1523	11.	AK002401
8	739.8	64.6	890	14	BQ962523
9	728	63.5	890	14	BQ941482
10	720.6	62.9	808	13	B1256255
11	693	60.5	880	13	BG289921
12	664	57.9	935	12	BG286300
13	652.8	57.0	812	12	BG035606
14	640	55.8	649	14	BQ68373
15	635.6	55.5	875	12	BE869129
16	629.6	54.9	916	12	BG167682
17	620.8	54.2	720	9	AU117376
18	607.4	53.0	748	9	AU126425
19	605.8	52.9	713	10	AV714754
20	588.8	49.6	729	13	B1550388
21	581.6	49.0	690	13	BF205467
22	535.6	48.5	938	10	BE202419
23	547.8	47.8	937	12	BG165573
24	547.4	47.8	701	12	BE238582
25	546	47.6	914	12	BF796706
26	545.6	47.6	672	14	BM714377
27	545.6	47.6	823	14	BM723657
28	520.2	45.4	930	12	BG170144
29	509.6	44.5	829	12	BG708726
30	509.4	44.5	693	12	BG779839
31	501.8	43.8	842	13	B1101933
32	481.8	42.0	705	13	B1597403
33	475.6	41.5	838	9	AL571115
34	464.4	40.5	712	9	A1796120
35	443.2	38.7	771	13	B1219641
36	442.6	38.6	658	9	AL710886
37	441	38.5	865	12	BG173981
38	437.6	38.2	444	12	BF858135
39	437.4	38.2	641	14	BM829952
40	434.2	37.6	772	13	BG971046
41	431.0	37.7	796	13	BG970128
42	429.6	37.5	567	12	BF857760
43	429.4	37.5	453	12	BF858139
44	427.8	37.3	519	12	BF857747
45	427.4	37.3	562	12	BF857755

ALIGNMENTS

RESULT 1
LOCUS AL558928 968 bp mRNA linear EST 16-FEB-2001
DEFINITION AL558928 LFI_NFL008_TC2 Homo sapiens CDNA clone CS0DJ007Y107 5
ACCESSION AL558928
VERSION AL558928.1 GI:12903928
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
JOURNAL Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..968
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ007Y107"
/clone_1ib="LFI_NFL008_TC2"
/sex="male"
/issue_type="T" cells from T cell leukemia"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand CDNA

QY 450 GCTGACTTCTGCTGGTGGCCCTTATGTGTGCTACTGGGCAATTATTAAGCTCTTTTGA 509
 Db 301 GCGTACTTTCCTGGTGGGCGCTTATGTGTGCTACTGGGCAATTATTAAGCTCTTTTGA 360
 QY 510 CCGCACACGCACTGCGAAGGTCAGTCAATGTGATGCAAAATATGTGTGAAGAACACACATA 569
 Db 361 CCGCACACGCACTGCGAAGGTCAGTCAATGTGATGCAAAATATGTGTGAAGAACACACATA 420
 QY 570 TTTAAGTCTTTTCTGTGGAAAACTGAGAAATCGAGTGTGTGGGAACACCTCTGAGAGACA 629
 Db 421 TTTAAGTCTTTTCTGTGGAAAACTGAGAAATCGAGTGTGTGGGAACACCTCTGAGAGACA 480
 QY 630 GAACATGTGTGATGTGTGGAGCACTTCTATACGACTTACAGACACCAATATGGGAAT 689
 Db 481 GAACATGTGTGATGTGTGGAGCACTTCTATACGACTTACAGACACCAATATGGGAAT 540
 QY 690 CATGGCTGTGTGGAGCACTTACAAACCCAGTTCAGAGCTGTGTATCAAGAGACTTGGACT 749
 Db 541 CATGGCTGTGTGGAGCACTTACAAACCCAGTTCAGAGCTGTGTATCAAGAGACTTGGACT 600
 QY 750 AAAGTCTGATGAACCTTCCCAATCAGATGACATGTGATGATGGCCAGAAATGAAGAAGA 809
 Db 601 AAAGTCTGATGAACCTTCCCAATCAGATGACATGTGATGATGGCCAGAAATGAAGAAGA 660
 QY 810 GTTTCAGATGTATTTTGCAAGAAGACGAGAGAGTGTCTAAATCTTTGACGGCAC 869
 Db 661 GTTTCAGATGTATTTTGCAAGAAGACGAGAGAGTGTCTAAATCTTTGACGGCAC 720
 QY 870 AGATGCTGTGTGACTCCGTTCTGACTTTTGAGAGAGTGTTCATCATGATCACAACAA 929
 Db 721 AGATGCTGTGTGACTCCGTTCTGACTTTTGAGAGAGTGTTCATCATGATCACAACAA 780
 QY 930 GGAACGGGGCTGCTTATATCAGCAGTGAAGAGAGAGAC - GTGAGCCCCCGCCCTGCAGACTC 988
 Db 781 GGAACGGGG - CTCGTTATATCAGCAGTGAAGAGAGAGAGAGAGCCCCCGCCCTGCAGACTC 838
 QY 989 TGCCTTTAAACACCCCGCATCCCTCTTTCATAAAGGATCTTTTATGTGAGAGACACA 1048
 Db 839 GGTGTGTTAAACACCCCGCATCCCTCTTTCATAAAGGATCTTTTATGTGAGAGACACA 898
 QY 1049 CTGAGGAGATATCTTGAAGAAATTTGATTCAGCGG 1082
 Db 899 CTGAGGAGATATCTTGAAGAAATTTGATTCAGCGG 932

RESULT 3
 LOCUS AL551698 842 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL551698 L71_NFL006_PL2 Homo sapiens cDNA clone CSOD1062YP05 5 prime, mRNA sequence.
 ACCESSION AL551698
 VERSION AL551698.1 GI:12889898
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 842)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope, Centre National de Sequencage
 BP 101 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 Location/Qualifiers
 1..842
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSOD1062YP05"
 /clone_11b="L71_NFL006_PL2"
 /issue_type="Placenta"
 /note="Vector: pcwvSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@life.com
 http://fulllength.invitrogen.com"

BASE COUNT 189 a 197 c 247 g 198 t 11 others
 ORIGIN

Query Match 70.9%; Score 812.8; DB 9; Length 842;
 Best Local Similarity 97.9%; Pred. No. 4.4e-218;
 Matches 822; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 1 ATGGCATGCGAGGCACTCTGCTGTGAGACTGTCCGGCTTGGCCCGCGCTTCTGT 60
 Db 4 ATGGCATGCGAGGCACTCTGCTGTGAGACTGTCCGGCTTGGCCCGCGCTTCTGT 63
 QY 61 GCTATGCTCTGCTGACCTTGGGGGCGGTGTGTACGCGTGTGACCGCGCGCTCCCG 120
 Db 64 GCTATGCTCTGCTGACCTTGGGGGCGGTGTGTACGCGTGTGACCGCGCGCTCCCG 123
 QY 121 TACGACGTGACCCGCTTGGGCGGCGCAAGCCCTGCTAGTCTGTGACCTGAAGCCG 180
 Db 124 TACGACGTGACCCGCTTGGGCGGCGCAAGCCCTGCTAGTCTGTGACCTGAAGCCG 183
 QY 181 CCGGGAGCGCGCGTGTGCGCGCTGTGTCAAGCGGTGATGTGTGTGAGACCCCTTC 240
 Db 184 CCGGGAGCGCGCGTGTGCGCGCTGTGTCAAGCGGTGATGTGTGTGAGACCCCTTC 243
 QY 241 CCGCGCGGTGTGATGAGAAATCTCAGCTGGGCGCGAGATTTGTGCAAGCGGAAATCCA 300
 Db 244 CCGCGCGGTGTGATGAGAAATCTCAGCTGGGCGCGAGATTTGTGCAAGCGGAAATCCA 303
 QY 301 AGCTTATTTTGGCAGGCTGATGATTTGGCAGTGAAGATCTTCCGCTTATAGCT 360
 Db 304 AGCTTATTTTGGCAGGCTGATGATTTGGCAGTGAAGATCTTCCGCTTATAGCT 363
 QY 361 GGCACGATATCAACTATTTGGCTTGTCAAGTGTCTCAAAAATTTGGCAGAAAGTGT 420
 Db 364 GGCACGATATCAACTATTTGGCTTGTCAAGTGTCTCAAAAATTTGGCAGAAAGTGT 423
 QY 421 GAGATCCGTATGCCCGCGGTGAAATCTCTGCTGACTTGTGCTGTGTATGTGT 480
 Db 424 GAGATCCGTATGCCCGCGGTGAAATCTCTGCTGACTTGTGCTGTGTATGTGT 483
 QY 481 GCACGTGGCATTTATATGCTCTTTTGGACCGCACAGCAGCTGCGAAGGGTCAGTCT 540
 Db 484 GCACGTGGCATTTATATGCTCTTTTGGACCGCACAGCAGCTGCGAAGGGTCAGTCT 543
 QY 541 GATGCAATATGTGTGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 600
 Db 544 GATGCAATATGTGTGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 603
 QY 601 TCGAGTGTGTGGAAGCACTCGAGAGACAGAACATGTTGATGTGAGAGACCTTCTAT 660
 Db 604 TCGAGTGTGTGGAAGCACTCGAGAGACAGAACATGTTGATGTGAGAGACCTTCTAT 663
 QY 661 ACGACTTACAGAGACAGATGGGGAATTCATGCTGTGGAGCAATGAAACCCAGTTC 720
 Db 664 ACGACTTACAGAGACAGATGGGGAATTCATGCTGTGGAGCAATGAAACCCAGTTC 723
 QY 721 TACGAGCTGTGATCAAAAGACTTGGACTTGAATGTGATGACTTCCCAATGAGTACG 780
 Db 724 TACGAGCTGTGATCAAAAGACTTGGACTTGAATGTGATGACTTCCCAATGAGTACG 783
 QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGAAAGAGAGAG 840
 Db 784 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTTGCAGAAAGAGAGAG 842

LOCUS	AL545355	824 bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AL545355 LTR1.NFL006.PL2 Homo sapiens cDNA clone CS0102YJ12 5 prime, mRNA sequence.				
ACCESSION	AL545355				
VERSION	AL545355.1	GI:12877836			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	unpublished (2001)				
COMMENT	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	BP 191 91006 Evry cedex - France				
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
FEATURES	Location/Qualifiers				
source	1..824				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="CS0102YJ12"				
	/clone_lib="LTR.NFL006.PL2"				
	/issue_type="placenta"				
	/note="Vector: pCMVSPORT 6; site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	176 a 191 c 257 g 198 t				
ORIGIN					
	69.5%; Score 796.4; DB 9; Length 824;				
Query Match	Best Local Similarity 99.2%; Pred. No. 1.9e-213;				
Matches	819; Conservative 2; Mismatches 3; Indels 2; Gaps 2;				
OY	6 ACTGCAGGCGATCTCGTCGTGAGACTCTCCGGCCCGGGCCGGTCTGTGCTAT 65				
Db	1 ACTGCAGGCGATCTCGTCGTGAGACTCTCCGGCCCGGGCCGGTCTGTGCTAT 60				
OY	66 GGTCTGTGCTACCTTCGGGGGGCGGTGTGATACGCTGGACCGCCCGGCTCCCGTACGA 125				
Db	61 GGTCTGTGCTACCTTCGGGGGGCGGTGTGATACGCTGGACCGCCCGGCTCCCGTACGA 120				
OY	126 CGTGAGCGCTTGGGCGCCGGGCAAGCGCTCCCTAGTCTGTGACCTGAAGACCGCGGG 185				
Db	121 CGTGAGCGCTTGGGCGCCGGGCAAGCGCTCCCTAGTCTGTGACCTGAAGACCGCGGG 180				
OY	186 AGCCGCGTGTCTGGGGCGTCTGTGTCAAGCGGTGGATGTGCTGTGAAGCCCTTCCGCG 245				
Db	181 AGCCGCGTGTCTGGGGCGTCTGTGTCAAGCGGTGGATGTGCTGTGAAGCCCTTCCGCG 240				
OY	246 CGGTCTCATGTGAGAAACATCCACAGCTGGGCGCCAGAGATTTCTGACAGCGGAAATCCAAGCT 305				
Db	241 CGGTCTCATGTGAGAAACATCCACAGCTGGGCGCCAGAGATTTCTGACAGCGGAAATCCAAGCT 300				
OY	306 TATTTATCCACAGCGTGAATGTGATTTGGGCAAGACAGAGCTTCGCGTTAGTGGGCA 365				
Db	301 TATTTATCCACAGCGTGAATGTGATTTGGGCAAGACAGAGCTTCGCGTTAGTGGGCA 360				
OY	366 CGATATCAACTATTGTGGCTTTGTCAAGGTCTCTCAAAAATTGGCAGAGTGTGAGAA 425				
Db	361 CGATATCAACTATTGTGGCTTTGTCAAGGTCTCTCAAAAATTGGCAGAGTGTGAGAA 420				
OY	426 TCCGATACCCCCGCTGAATTCCTCTGGCTACTTTCCTGTGTGTGGCCCTTATGTGTGCACT 485				

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
Db	421	TTCCGATATGCCCGCTGAAATCTCTCGCTGACTTTGCTGGCTTGACCTTATCTGTGCAC	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Qy	486	GGGCAATTAATATGCGCTTTTGGACCGACACGACACTGGCAAGGGTCAGTCATTGATGC	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Db	481	GGGCAATTAATATGCGCTTTTGGACCGACACGACACTGGCAAGGGTCAGTCATTGATGC	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Qy	546	AAATATGGTGGGAAGGAACAGCATATTTAAGTCTTTTCTGTGTGAAAACCTCAGAAATCGAG	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Db	541	AAATATGGTGGGAAGGAACAGCATATTTAAGTCTTTTCTGTGTGAAAACCTCAGAAATCGAG	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Qy	606	TTGTGGGAAGACACCTCGAGGACAGACAACTGTTGGATGGTGGAGACACCTTTTATATACGC	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Db	601	TTGTGGGAAGACACCTCGAGGACAGACAACTGTTGGATGGTGGAGACACCTTTTATATACGC	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Qy	666	TTACAGGACAGCAGATGGGGGAATTCATGCGCTTTGGAGCAATATAGAA-COCATTTCTACGA	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Db	660	TTACAGGACAGCAGATGGGGGAATTCATGCGCTTTGGAGCAATATAGAA-COCATTTCTACGA	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Qy	726	GCTGCTGATCAAGAAGCACTTGAAGTCTGATGATGATGATGATGATGATGATGATGATGATG	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Db	719	GCTGCTGATCAAGAAGCACTTGAAGTCTGATGATGATGATGATGATGATGATGATGATGATG	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Qy	786	TGATGGCCAGCAATATGAGAAGCACTTGCATGATGATGATGATGATGATGATGATGATGATG	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
Db	779	TGATGGCCAGCAATATGAGAAGCACTTGCATGATGATGATGATGATGATGATGATGATGATG	AL555978	1	GI:12898227	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
RESULT 5													
LOCUS	AL555978	873 bp	MRNA	linear	EST 16-FEB-2001								
DEFINITION	AL555978	L1.NFL006_PL2	Homo sapiens	cdna	clone CS0DK010Y111								
ACCESSION	AL555978												
VERSION	AL555978.1	GI:12898227											
KEYWORDS	EST.												
SOURCE	human.												
ORGANISM	Homo sapiens												
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.												
AUTHORS	Li, W. B., Gruber, C., Jesssee, J. and Polayes, D.												
TITLE	Full-length cDNA libraries and normalization												
JOURNAL	Unpublished (2001)												
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.												
FEATURES	Location/Qualifiers												
Source	1. 873 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DK010Y111" /clone_lib="L1.NFL006_PL2" /tissue_type="placenta" /note="Vector: pCMVSPORT												

Db	64	ATGGCAGTCGACAGGGCACTCTCGTCTGGAGCGCTGTCGGACCTCGGCCCGCCGGGCGCTTTCGT	123
Qy	61	GGTAATGATCGAGCTGACTTCCGGGGCGGCTGTGGTACGCTGTGACCGGGCGGCTCCGCG	120
Db	124	GGTATGTCTCGGTGACTCTCGGGCGGGCTGTGGTACGCTGTGACCGGGCGGCGGCTCCGCG	183
Qy	121	TTCAGACGTGACCGCCTTGGGGCGGGGCAAGGCGTCTGTATGCTGTGGACTTCAAGCAGCCG	180
Db	184	TTCAGACGTGACCGCCTTGGGGCGGGGCAAGGCGTCTGTATGCTGTGGACTTCAAGCAGCCG	243
Qy	181	CGGGAGCGCGCGGTGCTGGCGGCTGTGTCAGAGCGGTGGATATGCTGCTGGACCTTC	240
Db	244	CGGGAGCGCGCGGTGCTGGCGGCTGTGTCAGAGCGGTGGATATGCTGCTGGACCTTC	303
Qy	241	CGCGCGGCTGTCATGGAGAACTCCACGTGGGGCCAGAGATTTCTGACGGGGAATAATCA	300
Db	304	CGCGCGGCTGTCATGGAGAACTCCACGTGGGGCCAGAGATTTCTGACGGGGAATAATCA	363
Qy	301	AGGCTTATTTATGCGAGGCTGAGTGGATTTTGGCCAGTCAGAGACTTCTGCGGGTTAGCT	360
Db	364	AGGCTTATTTATGCGAGGCTGAGTGGATTTTGGCCAGTCAGAGACTTCTGCGGGTTAGCT	423
Qy	361	GGCCACGATATCAACTATTTTGGCTTTGTACAGTCTTCTCTCAAAAATTGGCAGAGAGGT	420
Db	424	GGCCACGATATCAACTATTTTGGCTTTGTACAGTCTTCTCTCAAAAATTGGCAGAGAGGT	483
Qy	421	GAGAAATCCGATGCCCCCGCTGAAATCCTGGCTGACTTTCTGTGTTGGGCGCTTATGTG	480
Db	484	GAAATATCCGATGCCCCCGCTGAAATCCTGGCTGACTTTCTGTGTTGGGCGCTTATGTG	543
Qy	481	GGACATGGGCAAT-TTAAATGGCTTTTGTGACCGACACGCACTGGCAAGGGCAGAGTCAT	539
Db	544	GGACATGGGCAATATTAATGCTCTTTTGTGACCGACACGCACTGGCAAGGGCAGAGTCAT	603
Qy	540	TGATGCAAAATTTGGTGGAGAGAAACGCAATTTTAAGTTAGTTCTTTCTGTGGAAATCTCGAA	599
Db	604	TGATGCAAAATTTGGTGGAGAGAAACGCAATTTTAAGTTAGTTCTTTCTGTGTGAAATCTCGAA	663
Qy	600	ATCGAGTGTGGGAGAACACCTTCGAGACACAGACAAATTTGGATGGTGGAGCACTTTCTTA	659
Db	664	ATTGAGTCTGTGGGAGACACCTTCGAGACACAGACAAATTTGGATGGTGGAGCACTTTCTTA	723
Qy	660	TACGACTTACAGGACAGACAGATGGGGAAATTCATGCTGTGGAGCAATAGAACCCCAAGTT	719
Db	724	TACGACTTACAGGACAGACAGATGGGGAAATTCATGCTGTGGAGCAATAGAACCCCAAGTT	783
Qy	720	CTACGAGCTGCTGATCAAAAGCACTTGGACTTAACTGTATGATCACTTCCCATCTGATAGAG	779
Db	784	CTACGAGCTGCTGATCAAAAGCACTTGGACTTAACTGTATGATCACTTCCCATCTGATAGAG	843
Qy	780	CATGAGTATTTGGCCAGAAATAGAAAGAA 809	
Db	844	CATGAGTATTTGGCCAGAAATAGAAAGAA 873	
RESULT 6			
AL558977		888 bp	mRNA linear EST 16-FEB-2001
LOCUS	AL558977	1711..NFI008..TC2	Homo sapiens cDNA clone CS00J008YK07 5
DEFINITION			prime_rRNA sequence.
ACCESSION	AL558977		
VERSION	AL558977.1	GI:12904022	
KEYWORDS	EST.		
SOURCE	human		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 888)		
JOURNAL	Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization		
UNPUBLISHED	Unpublished (2001)		
CONTACT	Contact: Genoscope		

Genoscope - Centre National de Sequencage									
BP 191 91006 EVRY cedex - France									
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.									
FEATURES									
source									
1..888									
/organism="Homo sapiens"									
/db_xref="taxon:9606"									
/clone="GSDJ0084K07"									
/clone_lib="LTI_NFL008_Tc2"									
/sex="male"									
/tissue_type="T cells from T cell leukemia"									
/note="Vector: pcmsport 6, site 1. NotI: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pcmsport 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filangeli@invitrogen.com URL : http://fulllength.invitrogen.com"									
BASE COUNT 180 a 213 c 281 g 209 t 5 others									
ORIGIN									
Query Match 68.7%; Score 787.2; DB 9; Length 888;									
Best Local Similarity 99.1%; Pval.No. 7.5e-211;									
Matches 797; Conservative 4; Mismatch 2; Indels 1; Gaps 1;									
Oy	1	ATGGCACTGCAAGGCACTCTGGTCGTGAGCGTCGCCGCTGCCGCCGCCGCTGTGT	60						
Db	85	ATGGCACTGCAAGGCACTCTGGTCATGAGCGTCGCCGCTGCCGCCGCCGCTGTGT	144						
Oy	61	GCATAGTCCTCGGCTGACTCGGGGCGCGTGGTAGCGCTGACCGCGGCCGCCG	120						
Db	145	GCATAGTCCTCGGCTGACTCGGGGCGCGTGGTAGCGCTGACCGCGGCCGCCG	204						
Oy	121	TACGAGCTGACGCGCTTGGGCGGGGCAAGCGCTGCTAGCTGGACCTGACACGCG	180						
Db	205	TACGAGCTGACGCGCTTGGGCGGGGCAAGCGCTGCTAGCTGGACCTGACACGCG	264						
Oy	181	CGGGAGCGCGCGCTGCGGGGCTGTGCGAAGCGCGGATGCTGTGACGCGCTTC	240						
Db	265	CGGGAGCGCGCGCTGCGGGGCTGTGCGAAGCGCGGATGCTGTGAGGCGCTTC	324						
Oy	241	CGCGCGGGTGTGATGAGAAATCTCAGCTGGGCCACAGATTCGTGCGGGGAAATCTCA	300						
Db	325	CGCGCGGGTGTGATGAGAAATCTCAGCTGGGCCACAGATTCGTGACGGGGAAATCTCA	384						
Oy	301	AGCGTTATTTATGCGACGCTGATGATTTGGCCAGTCAGAGAACTTCCTGCCGTTAGCT	360						
Db	385	AGCGTTATTTATGCGACGCTGATGATTTGGCCAGTCAGAGAACTTCCTGCCGTTAGCT	444						
Oy	361	GGCCAGCATATCACTATTGGCTTTGTTCAGGTCTTCTCTCAAAATTTGGCAGAAGTGT	420						
Db	445	GGCCAGCATATCACTATTGGCTTTGTTCAGGTCTTCTCTCAAAATTTGGCAGAAGTGT	504						
Oy	421	GAGAAATCGTATGCCCCCGGTGATATCCCGGCTGACTTTCTGTGTGGGCGCTTATGTGT	480						
Db	505	GAGAAATCGTATGCCCCCGGTGATATCCCGGCTGACTTTCTGTGTGGGCGCTTATGTGT	564						
Oy	481	GCAGTGGGCAATTAATAGGCTCTTTTTCACCGCACACGACGTGCGAAAGGTGACAGTATT	540						
Db	565	GCAGTGGGCAATTAATAGGCTCTTTTTCACCGCACACGACGTGCGAAAGGTGACAGTATT	624						
Oy	541	GATCGAATATATGCTGGAGAGACAGCATATTTAAGTCTTTTCTGTGGAAATCTCAGAA	600						
Db	625	GATCGAATATATGCTGGAGAGACAGCATATTTAAGTCTTTTCTGTGGAAATCTCAGAA	684						
Oy	601	TGCACTGTGTGGAGACCTCGAGACAGCAATGTTGATGTGTGAGCACCTTTCTAT	660						
Db	685	TGCACTGTGTGGAGACCTCGAGACAGCAATGTTGATGTGTGAGCACCTTTCTAT	744						
Oy	661	ACGACTTTCAGAGACAGCATGAGGGAATTTCTATGCGCTG-TTGGAGCAATAGAACCCCGATT	719						


```

polyA_signal 1500..1505
                /gene="Amacr"
                /note="putative"
polyA_site 1523
            /gene="Amacr"
            /note="putative"
BASE COUNT 365 a 386 c 414 g 358 t
ORIGIN
Query Match 66.4%; Score 760.4; DB 11; Length 1523;
Best Local Similarity 79.6%; Pred. No. 3.4e-203;
Matches 912; Conservative 0; Mismatches 231; Indels 3; Gaps 1;

QY 1 ATGCACCTGCAGGACATCTGCTGCTGAGAGCTGTCGCCGCGCCGCGCCGCTCTGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23 ATGGTGTGCTGCGGCTGCAGAGGTTGTGAGCTGGCAGGCTGGCCCGGGCCGTTCTGC 82

QY 61 GCTATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 83 GGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 139

QY 121 TAGACGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 140 ACGGCGCAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199

QY 181 CGGGGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 CAGGAGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259

QY 241 CGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 260 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319

QY 301 AGGCTTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 320 AAGCTCATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 379

QY 361 GGGCAGCATATCAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 380 GGGCATGACATCAATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439

QY 421 GAGAAATCCGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 440 GAGAAATCCGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 499

QY 481 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559

QY 541 GATCCAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 560 GATCCAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619

QY 601 TCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 620 ATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679

QY 661 ACGATTCACGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 680 ACAACCTACGAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739

QY 721 TACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 740 TATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799

QY 781 ATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 800 TCACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859

QY 841 GCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 860 GCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919

```

```

QY 901 GAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 920 GAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979

QY 961 CAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 980 CAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039

QY 1021 AAAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1040 AAAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1099

QY 1081 CGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1100 CAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159

QY 1141 AGCTTC 1146
    | | | | |
DB 1160 AATCTC 1165

RESULT 8
BO962523
LOCUS BO962523
DEFINITION BO962523 890 bp mRNA linear EST 21-AUG-2002
ACCESSION AGENCOURT_881570 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5379327
VERSION BO962523
KEYWORDS BO962523.1 GI:22378001
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 890)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gcrabs-femail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCW2566 row: c column: 08
High quality sequence stop: 750.
Location/Qualifiers
1..890
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH-MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="PH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pORF7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming;
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCACGAG(5). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."
BASE COUNT 187 a 221 c 278 g 203 t
ORIGIN
Query Match 64.6%; Score 739.8; DB 14; Length 890;
Best Local Similarity 99.1%; Pred. No. 1.8e-197;
Matches 744; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCAGTGCAGGAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60

```

```

|||||
Db 43 ATGGGACATGACGGGATCTCGGTCATGAGAGCTGTCCGGCCCTGGCCCCCGGGCCGTTCTGT 102
QY 61 GCTATGGTCGCGGGGACTTGGGGGGCGGTGGAGCGGTGGAGCCGGCCGGCGCCG 120
Db 103 GCTATGGTCGCGGGGACTTGGGGGGCGGTGGAGCGGTGGAGCCGGCCGGCGCCG 162
QY 121 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTGCTAGTGTGCTGGACCTGAAGCAGCG 180
Db 163 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTGCTAGTGTGCTGGACCTGAAGCAGCG 222
QY 181 CGGGGAGCGCGCGTCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTCTGGAGCCCTTC 240
Db 223 CGGGGAGCGCGCGTCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTCTGGAGCCCTTC 282
QY 241 CGCGCGGCTGTATGAGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGGAATAATCCA 300
Db 283 CGCGCGGCTGTATGAGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGGAATAATCCA 342
QY 301 AGGCTATTATATGCCAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 343 AGGCTATTATATGCCAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 402
QY 361 GGGCAGATATCACTATTGGCTTTGTGACAGTGTCTCTCAAAAATTGGCAGAAAGTGT 420
Db 403 GGGCAGATATCACTATTGGCTTTGTGACAGTGTCTCTCAAAAATTGGCAGAAAGTGT 462
QY 421 GAGAATCCGATATGCCCCGCTGATCTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 463 GAGAATCCGATATGCCCCGCTGATCTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCT 522
QY 481 GCACTGGGCAATATATATGCTCTTTTGTGACCGCACGCACTGGCAGAGGCTGACGTCAT 540
Db 523 GCACCTGGGCAATATATATGCTCTTTTGTGACCGCACGCACTGGCAGAGGCTGACGTCAT 582
QY 541 GATGCAATATATGCTGGAGGAAAGCAATATTAAGTCTTCTGCTGGAATAACTGAGAA 600
Db 583 GATGCAATATATGCTGGAGGAAAGCAATATTAAGTCTTCTGCTGGAATAACTGAGAA 642
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGATGATGATGATGATGATGATGAT 660
Db 643 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGATGATGATGATGATGATGATGAT 702
QY 661 ACAGCTTACAGAGACAGCAGATGGGGAATTCATGCTGTTGAGACATATGAACCCAGTTC 720
Db 703 ACAGCTTACAGAGACAGCAGATGGGGAATTCATGCTGTTGAGACATATGAACCCAGTTC 762
QY 721 TACGAGCTGTGATCAAGGACTTGGACTAA 751
Db 763 TACGAGCTGTGATCAAGGACTTGGGAGAA 793

RESULT 9
BO941482 890 bp mRNA linear EST 21-AUG-2002
LOCUS BO941482
DEFINITION AGNCOURT_8821476 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6203684 5', mRNA sequence.
ACCESSION BO941482
VERSION BO941482.1 GI:22356960
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgsb@rttmail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

```

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: LHAM3623 row: 1 column: 21
 High quality sequence stop: 621.

FEATURES

source

Location/Qualifiers
 1..890
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6203684"
 /clone_lib="Lupski_sciatic_nerve"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH108"
 /note="Vector: pCMV-Sport6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGCGTCG-3' and
 5'-GACTAGTTCATAGATCGCGCGCCGCT(15)-3'. Size selected >
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

BASE COUNT 253 a 189 c 219 g 223 t 6 others
 ORIGIN

Query Match 63.5%; Score 728; DB 14; Length 890;
 Best Local Similarity 99.2%; Pred. No. 3.8e-194;

Matches 731; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY 396 TCTCCAAAATTTGGCAGAGTGTGAGAAATCCGATGCCCCGCTGATCTCTGCTGA 455
Db 1 TCTCCAAAATTTGGCAGAGTGTGAGAAATCCGATGCCCCGCTGATCTCTGCTGA 60
QY 456 CTTTCTGCTGTGTGCTTATGTGTGCACTGGCATTATTAATGCTCTTTTGAACCGCAG 515
Db 61 CTTTCTGCTGTGTGCTTATGTGTGCACTGGCATTATTAATGCTCTTTTGAACCGCAG 120
QY 516 ACCGACCTGGCAAGGTCAGTGCATTGATGCAAAATATGTTGGAAGAACAGCATATTTAAG 575
Db 121 ACCGACCTGGCAAGGTCAGTGCATTGATGCAAAATATGTTGGAAGAACAGCATATTTAAG 180
QY 576 TTCTTTTCTGTGAAAATCTCAAAATCAGTCTGTGGGAACACCTCGAGAGACAGAAAT 635
Db 181 TTCTTTTCTGTGAAAATCTCAAAATCAGTCTGTGGGAACACCTCGAGAGACAGAAAT 240
QY 636 GTTGGAGTGTGAGACCTTTCTATAGCATTACAGACAGCAGATGGGGAATTCATGGC 695
Db 241 GTTGGAGTGTGAGACCTTTCTATAGCATTACAGACAGCAGATGGGGAATTCATGGC 300
QY 696 TGTGGAGCAATPAGAACCCCAAGTCTACGACTGCTGTATCAAGGACTTGGACTAAAGTC 755
Db 301 TGTGGAGCAATPAGAACCCCAAGTCTACGACTGCTGTATCAAGGACTTGGACTAAAGTC 360
QY 756 TGATGAACCTTCCCATCAGATGAGCATGATTTGGCCAGAAATGAAGAAGAAATTTCG 815
Db 361 TGATGAACCTTCCCATCAGATGAGCATGATTTGGCCAGAAATGAAGAAGAAATTTCG 420
QY 876 CTGTGTGACCTCGGCTTGTGACTTTTGAAGAGTGTTCATATGATCAACAAGAAAGC 935
Db 481 CTGTGTGACCTCGGCTTGTGACTTTTGAAGAGTGTTCATATGATCAACAAGAAAGC 540
QY 936 GGGCTCGTTTATCAACCATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 995
Db 541 GGGCTCGTTTATCAACCATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

```

Oy	996	AAACACCAGCAGCATCCCTCTTTTCAAAAGCATCTTTCAAGAGAACACACTGAGGA	1055
Db	601	AAACACCAGCAGCATCCCTCTTTTCAAAAGCATCTTTCAAGAGAACACACTGAGGA	660
Oy	1056	GATACCTGAAGATTTGGATTGACGGCCGAGAGATTATTCAGCTTACAGTAAAT	1115
Db	661	GATACCTGAAGATTTGGATTGACGGCCGAGAGATTATTCAGCTTACAGTAAAT	720
Oy	1116	CATTGAAGTATTAAGG	1132
Db	721	CATTGAAGTATTAAGG	737
RESULT 10			
LOCUS	BI236255	808 bp	mRNA
DEFINITION	60297507561 NIH_MGC_12 Homo sapiens	cdna clone IMAGE:5114130 5',	
ACCESSION	BI236255		
VERSION	BI236255.1	GI:14810488	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgi.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: csapbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: Incyte Genomics, Inc.		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LHAM1277 row: f column: 19		
	High quality sequence stop: 751.		
FEATURES			
source			
	1..808		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5114130"		
	/clone_1db="NIH_MGC_12"		
	/tissue_type="cervical carcinoma cell line"		
	/lab_host="DH10B"		
	/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI;		
	Site-2: SalI; Cloned unidirectionally. Primer: Oligo dT.		
	Average insert size 1.4 kb. Library prepared by Life		
	Technologies."		
BASE COUNT	174 a	189 c	253 g
ORIGIN	192 t		
Query Match	62.9%; Score 720.6; DB 13; Length 808;		
Best Local Similarity	98.1%; Pred. No. 4.5e-192;		
Matches 792; Conservative	0; Mismatches 9; Indels 6; Gaps 6;		
Oy	28	GACCTCTCCGCGCCGCGCGCGCGCTGTGCTAGTGCCTGCGACTTGGGGCG	87
Db	1	GACCTCTCCGCGCGCGCGCGCGCGCTGTGCTAGTGCCTGCGACTTGGGGCG	60
Oy	88	CGGTGTGACGGGTGACCGCGCGCGCTCCCGCTACGAGCTAGCCGCTTGGCGGGGC	147
Db	61	CGGTGTGACGGGTGACCGCGCGCGCTCCCGCTACGAGCTAGCCGCTTGGCGGGGC	120
Oy	148	AAGCGTGCCTAGTCTGACCTGAACACCGCGGGAGCGCGCTGCTGGCGGTCTG	207
Db	121	AAGCGTGCCTAGTCTGACCTGAACACCGCGGGAGCGCGCTGCTGGCGGTCTG	180
Oy	208	TGCAGCGGTGCGATGTCTGTGAGCCCTTCGCGCGGCGTGTATGAGAGAACTCCAG	267
FEATURES			
source			
	1..880		
	/organism="Homo sapiens"		

/db.xref="taxon:9606"
 /clone_id="NIH_MGC_93"
 /tissue_type="transitional cell papilloma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: bladder; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.7 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 180 a 235 c 270 g 195 t
 ORIGIN

Query Match 60.5%; Score 693; DB 12; Length 880;
 Best Local Similarity 97.4%; Pred. No. 2.8e-184;
 Matches 737; Conservative 0; Mismatches 15; Indels 5; Gaps 3;

QY 1 ATGGCACTGCAGGAGCATTCGGCTGTGAGAGCTCCGGCCCGGCGCCGTTCTGT 60
 DB 42 ATGGCACTGCAGGAGCATTCGGCTGTGAGAGCTCCGGCCCGGCGCCGTTCTGT 101
 QY 61 GCTATGTCCTGCTGACTTGGGGCGCGTGTGTACCGCTGAGACCGCGGCTCCGC 120
 DB 102 GCTATGTCCTGCTGACTTGGGGCGCGTGTGTACCGCTGAGACCGCGGCTCCGC 161
 QY 121 TACGACGTGACCGCTTGGGGCGCGTGTGTACCGCTGAGACCGCGGCTCCGC 180
 DB 162 TACGACGTGACCGCTTGGGGCGCGTGTGTACCGCTGAGACCGCGGCTCCGC 221
 QY 181 CGGGAGCGCGCGCTGCTGCGGCTGTGTACCGCTGAGACCGCTGAGACCGCTTC 240
 DB 222 CGGGAGCGCGCGCTGCTGCGGCTGTGTACCGCTGAGACCGCTGAGACCGCTTC 281
 QY 241 CGCGCGGCTGTGTACGAGAACTCCAGCTGGGCCGAGATTTCTGCACGCGGAAATCCA 300
 DB 282 CGCGCGGCTGTGTACGAGAACTCCAGCTGGGCCGAGATTTCTGCACGCGGAAATCCA 341
 QY 301 AGGCTATTATTCAGAGCTAGTGTGATTTGGCCAGTACGAGACCTTCCCGGTTACT 360
 DB 342 AGGCTATTATTCAGAGCTAGTGTGATTTGGCCAGTACGAGACCTTCCCGGTTACT 401
 QY 361 GGGCAGATATCACTATTGGCTTTTGCAGGTGTCTCTCAAAAATTTGGCAGAGTGT 420
 DB 402 GGGCAGATATCACTATTGGCTTTTGCAGGTGTCTCTCAAAAATTTGGCAGAGTGT 461
 QY 421 GAGAATCCGATGCCCGCTGATTCCTGCTGCTGATTCCTGCTGCTGCTGCTGCT 480
 DB 462 GAGAATCCGATGCCCGCTGATTCCTGCTGCTGATTCCTGCTGCTGCTGCTGCT 521
 QY 481 GCATGGGCAATTATATGGCTTTTGTACCGCAGCAGCTGGCAAGGTCAGTCAAT 540
 DB 522 GCATGGGCAATTATATGGCTTTTGTACCGCAGCAGCTGGCAAGGTCAGTCAAT 581
 QY 541 GATCAAAATATGTGAGAGAAACAGCATATTAGTTCTTTTGTGAAAATTCAGAAA 600
 DB 582 GATCAAAATATGTGAGAGAAACAGCATATTAGTTCTTTTGTGAAAATTCAGAAA 641
 QY 601 TCGAGTCTGTGGAGAACCTCGAGAGCAGAACTGTGG-ATGGTGGAGCAGCTTTCTA 659
 DB 642 TCGAGTCTGTGGAGAACCTCGAGAGCAGAACTGTGGTGGTGGAGCAGCTTTCTA 701
 QY 660 TACGACTTACGAGACAGATGGGG--AATTCATGGCTTTGGAG-CAATAGAACCC 715
 DB 702 TACGACTTACGAGACAGATGGGGCAATTCATGGCTGATGAGCAGCTAGAACCC 761
 QY 716 AGTTCTACGAGCTGCTGATCAAGGACTTGGACTAAA 752
 DB 762 AAGTCTACGAGCTGCTGATCAAGGACTTGGCTAAA 798

RESULT 12
 BG286300 935 bp mRNA linear EST 21-FEB-2001
 LOCUS BG286300

DEFINITION 602382457F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:449990 5',
 mRNA sequence.
 ACCESSION BG286300
 VERSION BG286300.1 GI:13039052
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 935)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LHAM10365 row: a column: 15
 High quality sequence start: 4
 High quality sequence stop: 701.
 Location/Qualifiers

FEATURES
 source
 1. 935
 /organism="Homo sapiens"
 /db.xref="taxon:9606"
 /clone_id="NIH_MGC_93"
 /tissue_type="transitional cell papilloma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: bladder; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.7 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 190 a 246 c 299 g 200 t
 ORIGIN

Query Match 57.9%; Score 664; DB 12; Length 935;
 Best Local Similarity 96.1%; Pred. No. 4.4e-176;
 Matches 713; Conservative 0; Mismatches 25; Indels 4; Gaps 3;

QY 1 ATGGCACTGCAGGAGCATTCGGCTGTGAGAGCTCCGGCCCGGCGCCGTTCTGT 60
 DB 28 ATGGCACTGCAGGAGCATTCGGCTGTGAGAGCTCCGGCCCGGCGCCGTTCTGT 87
 QY 61 GCTATGTCCTGCTGACTTGGGGCGCGTGTGTACCGCTGAGACCGCGGCTCCGC 120
 DB 88 GCTATGTCCTGCTGACTTGGGGCGCGTGTGTACCGCTGAGACCGCGGCTCCGC 147
 QY 121 TACGACGTGACCGCTTGGGGCGCGTGTGTACCGCTGAGACCGCTGAGACCGCG 180
 DB 148 TACGACGTGACCGCTTGGGGCGCGTGTGTACCGCTGAGACCGCTGAGACCGCG 207
 QY 181 CGGGAGCGCGCGCTGCTGCGGCTGTGTACCGCTGAGACCGCTGAGACCGCTTC 240
 DB 208 CGGGAGCGCGCGCTGCTGCGGCTGTGTACCGCTGAGACCGCTGAGACCGCTTC 267
 QY 241 CGCGCGGCTGTGTACGAGAACTCCAGCTGGGCCAGAGATTTGACAGCGGAAATCCA 300
 DB 268 CGCGCGGCTGTGTACGAGAACTCCAGCTGGGCCAGAGATTTGACAGCGGAAATCCA 327
 QY 301 AGGCTATTATTCAGAGCTAGTGTGATTTGGCCAGTACGAGACCTTCCCGGTTAGCT 360
 DB 328 AGGCTATTATTCAGAGCTAGTGTGATTTGGCCAGTACGAGACCTTCCCGGTTAGCT 387
 QY 361 GGGCAGATATCACTATTGGCTTTTGCAGGTGTCTCTCAAAAATTTGGCAGAGTGT 420
 DB 388 GGGCAGATATCACTATTGGCTTTTGCAGGTGTCTCTCAAAAATTTGGCAGAGTGT 447

QY	421	GAAATACCGTATAGCCCGCGTGAATCCGCGTGCACCTTTCCTGTCGTAGCCCTATATGT	480
Db	448	GAAATACCGTATAGCCCGCGTGAATCCGCGTGCACCTTTCCTGTCGTAGCCCTATATGT	507
QY	481	GCACGTGGGCAATTATATAGTCTTTTATGACCGGACACGACGTGGCAAGGTCACGTCAAT	540
Db	508	GCACGTGGGCAATTATATAGTCTTTTATGACCGGACACGACGTGGCAAGGTCACGTCAAT	567
QY	541	GATGCAATATGTGTGGGAAGAACACATATTTAACTCTTTTCTGTGAAAAATCAGAAA	600
Db	568	TGATGCAATATGTGTGGGAAGAACACATATTTAACTCTTTTCTGTGAAAAATCAGAAA	627
QY	601	TGCAGTCTGTGTGGGAAGACACTCGAGAC-AGAACATGTGTGATGTGTGAGACACCTTCT	658
Db	628	TGCAGTCTGTGTGGGAAGACACTCGAGACACGACACCATGTGTGTGTGTGAGACACCTTCT	687
QY	659	ATACGACTTACAGACAC-GCAGATGGGGATTTCAATGCTCTTGTGAGCAATAGAACCCAG	717
Db	688	ATACGACTTACAGACACGACAGATGGCGAATTTCAATGCTCTTGTGAGCAATAGAACCCAG	746
QY	718	TTTCTACGAGCTGCTGTATCAAG 739	
Db	747	TTTCTACGAGCTGCGATCAAG 768	
RESULT 13			
LOCUS	BG035606	812 bp	mRNA linear EST 24-JAN-2001
DEFINITION	602325670F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413833 5',		
ACCESSION	BG035606		
VERSION	BG035606.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.		
AUTHORS	1 (bases 1 to 812)		
TITLE	NIH-MGC http://mgi.nci.nih.gov/ .		
JOURNAL	Unpublished Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs@emell.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: Incyte Genomics distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L14M10140 row: k column: 18 High quality sequence stop: 672. Location/Qualifiers		
FEATURES			
source	1. 812		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4413833"		
	/clone_lib="NIH_MGC_90"		
	/tissue_type="adenocarcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: Liver; Vector: pCMV-SPORE6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."		
BASE COUNT	171 a 195 c 257 g 189 t		
ORIGIN			
Query Match	57.0%	Score 652.8;	DB 12; Length 812;
Best Local Similarity	99.8%	Pred: No. 6e-173;	
Matches 665:	Conservative 0;	Mismatches 2;	Indels 1; Gaps 1.
QY	1	ATGCGACTGACAGGCAATCTCGGTGTCGAGCTGTGCGGCTGCGGCGCCCGCTTCGT	60

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	8	ATGGACATCGAAGGCGATCTCGTCATGAGAGCTGTCCGGCTTGCCGCCCGGCGCGTTCTGT	67									
Oy	61	GCATATGCTCTCGCTGACTTTCGGGGGCGGTGGTACGCGTACGCGACGCGCGGTCCCGC	120									
Db	68	GCATATGCTCTCGCTGACTTTCGGGGGCGGTGGTACGCGTACGCGACGCGCGGTCCCGC	127									
Oy	121	TACGACGTGACCCCTTGGGCGCGGGCAACGGCTTCCTACTGCTGGACCTTACACAGCC	180									
Db	128	TACGACGTGACCCCTTGGGCGCGGGCAACGGCTTCCTACTGCTGGACCTTACACAGCC	187									
Oy	181	CGGGAGCCGCGCTGTCTGGCGGCTGTGTGCAAGCGTGGATGTGCTGTGAGCCCTTC	240									
Db	188	CGGGAGCCGCGCTGTCTGGCGGCTGTGTGCAAGCGTGGATGTGCTGTGAGCCCTTC	247									
Oy	241	CGCGCGGTGTATGAGAGAACTCCACGCTGGGCCCCAGAGATTCGTGACGGGAAAAATCCA	300									
Db	248	CGCGCGGTGTATGAGAGAACTCCACGCTGGGCCCCAGAGATTCGTGACGGGAAAAATCCA	307									
Oy	301	AGGCTATATTTATGCGACAGCTGAGTGTGATTTTGGCCAGTCAAGAACGCTTTCGCGGTTAGCT	360									
Db	308	AGGCTATATTTATGCGACAGCTGAGTGTGATTTTGGCCAGTCAAGAACGCTTTCGCGGTTAGCT	367									
Oy	361	GGCGACAGATCACTATTTGGCTTGTTCAGTCTTCTCTCAAAAATTTGGCAGAAAGTGT	420									
Db	368	GGCGACAGATCACTATTTGGCTTGTTCAGTCTTCTCTCAAAAATTTGGCAGAAAGTGT	427									
Oy	421	GACAAATCCGTATGCGCCCGCTGATTCCTCCGGGTGACTTTCGTTGGTGGCCCTTATGTG	480									
Db	428	GACAAATCCGTATGCGCCCGCTGATTCCTCCGGGTGACTTTCGTTGGTGGCCCTTATGTG	487									
Oy	481	GCACATCGCATTAATATAGGCTCTTTTGTACCGCACACGACATGACAAAGGTTCAGTCTAT	540									
Db	488	GCACATCGCATTAATATAGGCTCTTTTGTACCGCACACGACATGACAAAGGTTCAGTCTAT	547									
Oy	541	GATGCAATATGCTGTGGAGAGACAGATATTTAAGCTCTTTCTGTGAAAAATCACAATA	600									
Db	548	GATGCAATATGCTGTGGAGAGACAGATATTTAAGCTCTTTCTGTGAAAAATCACAATA	607									
Oy	601	TGCATGCTGTGTGGAGACACTCGAGACACGAACATGTTGGATGTGTGAGACACTTTCTAT	660									
Db	608	TGCATGCTGTGTGGAGACACTCGAGACACGAACATGTTGGATGTGTGAGACACTTTCTAT	666									
Oy	661	ACGACTTGA 668										
Db	667	ACGACTTGA 674										
RESULT 14												
LOCUS	B0638373	649 bp	mRNA	linear	EST 15-JUL-2002							
DEFINITION	hd21g09.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he											
ACCESSION	B0638373											
VERSION	B0638373.1											
KEYWORDS	EST.											
SOURCE	human.											
ORGANISM	human sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.											
AUTHORS	1 (bases 1 to 649)											
TITLE	Wistow G., Bernstein S.L., Wiat M.K., Ray S., Behal A., Touchman J.W., Bouffard G., Smith D. and Peterson K.											
JOURNAL	Expressed sequence tag analysis of human retina for the NIH/NIH project: Rebinidin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts											
COMMENT	Mol. Vis. 8 (4), (2002) In press											
	Contact: Wistow G.											
	Section on Molecular Structure and Function											
	National Eye Institute			</								


```

Db 300 TGGCAGGCTAGTGGATTGGCCAGTCTGCGGTTAGCTGGCCAGCATAT 359
OY 372 CAACTATTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGTGAGATCCGTA 431
Db 360 CAACTATTGGC-TGTCTAGGTGTTCTCTCAAAAATTGGCAGAGTGTGAGATCCGTA 418
OY 432 TGGCCGCTGAAATCTCCGCTGACTTTGCTGTGTGCGCTTATGTGTGACACTGGGCAT 491
Db 419 TGGCCGCTGAAATCTCCGCTGACTTTGCTGTGTGCGCTTATGTGTGACACTGGGCAT 478
OY 492 TATATGCTCTTTTGTGACCGCACGACATGGCAAGGTCAAGTCATGTGATCAAAATAT 551
Db 479 TATATGCTCTTTTGTGACCG-ACACGACATGACAAAGGTCAAGTCATGTGATCAAAATAT 537
OY 552 GGTGGAAGGAAGCATATTTAAGTTCTTTCTGTGAAAACTAGAAATGAGTCTGTG 611
Db 538 GGTGGAAGGAAGCATATTTAAGTTCTTTCTGTGAAAACTAGAAATGAGTCTGTG 597
OY 612 GGAAGCACTCGAGAGACAGACATGTGGA-TGGTGGAGCAGCTTCTATACGACTTACA 670
Db 598 GGAAGCACTCGAGAGACAGACATGTGGA-TGGTGGAGCAGCTTCTATACGACTTACA 657
OY 671 GGACAGCAGAT-GGGGAATTCATGGCTGTGAGCAATAGAACCCAGTT 719
Db 658 GGACAGCAGATGGGGAAATTCATGGGTGTGGCAATAGAACCCAGTT 707

```

Search completed: April 2, 2003, 02:22:44
 Job time : 1955.31 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 19:55:13 ; Search time 48.0076 Seconds
(without alignments)
7320.746 Million cell updates/sec

Title: US-09-967-305-3

Perfect score: 1146
Sequence: 1 atggcactgcagggccttc.....ataagtaaaagctagcttc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/p/odata1/1/ina/5A.COMB.seq:*
2: /cgn2_6/p/odata1/1/ina/5B.COMB.seq:*
3: /cgn2_6/p/odata1/1/ina/6A.COMB.seq:*
4: /cgn2_6/p/odata1/1/ina/6B.COMB.seq:*
5: /cgn2_6/p/odata1/1/ina/pctus.COMB.seq:*
6: /cgn2_6/p/odata1/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1142.8	99.7	1621	4 US-09-020-956-107	Sequence 107, App
2	1142.8	99.7	1621	4 US-09-030-607-107	Sequence 107, App
3	1142.8	99.7	1621	4 US-09-605-785-107	Sequence 107, App
4	1142.8	99.7	1621	4 US-09-439-313-107	Sequence 107, App
5	1142.8	99.7	1621	4 US-09-352-616A-107	Sequence 107, App
6	1142.8	99.7	1621	4 US-09-232-149A-107	Sequence 107, App
7	406.6	35.5	773	4 US-09-020-956-3	Sequence 3, App11
8	406.6	35.5	773	4 US-09-030-607-3	Sequence 3, App11
9	406.6	35.5	773	4 US-09-605-785-3	Sequence 3, App11
10	406.6	35.5	773	4 US-09-439-313-3	Sequence 3, App11
11	406.6	35.5	773	4 US-09-352-616A-3	Sequence 3, App11
12	406.6	35.5	773	4 US-09-232-149A-3	Sequence 3, App11
13	403.2	35.2	793	4 US-09-020-956-33	Sequence 33, App1
14	403.2	35.2	793	4 US-09-030-607-33	Sequence 33, App1
15	403.2	35.2	793	4 US-09-605-785-33	Sequence 33, App1
16	403.2	35.2	793	4 US-09-439-313-33	Sequence 33, App1
17	403.2	35.2	793	4 US-09-352-616A-33	Sequence 33, App1
18	403.2	35.2	793	4 US-09-232-149A-33	Sequence 33, App1
19	400.2	34.9	816	4 US-09-020-956-2	Sequence 2, App11
20	400.2	34.9	816	4 US-09-030-607-2	Sequence 2, App11
21	400.2	34.9	816	4 US-09-605-785-2	Sequence 2, App11
22	400.2	34.9	816	4 US-09-439-313-2	Sequence 2, App11
23	400.2	34.9	816	4 US-09-352-616A-2	Sequence 2, App11
24	400.2	34.9	816	4 US-09-232-149A-2	Sequence 2, App11
25	316.4	27.6	421	4 US-09-222-575-116	Sequence 116, App1
26	115	10.0	537	4 US-09-020-956-74	Sequence 74, App1
27	115	10.0	537	4 US-09-030-607-74	Sequence 74, App1

28	115	10.0	537	4 US-09-605-785-74	Sequence 74, App1
29	115	10.0	537	4 US-09-439-313-74	Sequence 74, App1
30	115	10.0	537	4 US-09-352-616A-74	Sequence 74, App1
31	115	10.0	537	4 US-09-232-149A-74	Sequence 74, App1
32	66.2	5.8	328	4 US-09-605-785-672	Sequence 672, App
33	47	4.1	1412	1 US-08-097-831-1	Sequence 1, App11
34	46	4.0	1143	4 US-09-655-270A-4	Sequence 4, App11
35	46	4.0	1203	4 US-09-651-941-4	Sequence 4, App11
36	46	4.0	1203	4 US-09-955-597-4	Sequence 4, App11
37	46	4.0	7218	1 US-08-232-163-14	Sequence 14, App1
38	46	4.0	12508	4 US-09-655-270A-1	Sequence 1, App11
39	46	4.0	12523	4 US-09-651-941-1	Sequence 1, App11
40	46	4.0	12523	4 US-09-955-597-1	Sequence 1, App11
41	44	3.8	2240	4 US-08-864-032A-37	Sequence 37, App1
42	40.4	3.5	2214	3 US-08-864-038A-1	Sequence 1, App11
43	40.4	3.5	3331	3 US-08-864-038A-2	Sequence 2, App11
44	40.4	3.5	3331	3 US-08-864-038A-3	Sequence 3, App11
45	40	3.5	529	4 US-09-159-106-14	Sequence 14, App1

ALIGNMENTS

```
RESULT 1
US-09-020-956-107
; Sequence 107, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Homo sapiens
; ORIGINAL SOURCE:
; US-09-020-956-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCCTTCGCTGAGCTGCCGCGGCGGCGCTTCTGT 60
DB 5 ATGGCACTGCAGGGCCTTCGCTGAGCTGCCGCGGCGGCGGCGCTTCTGT 64
```

QY 61 GCTATGTCCTGCTGACTTTCGGGGCGCTGTGTACGGCTGGACCGCCGGCTCCCG 120
 |||||||
 Db 65 GCTATGTCCTGCTGACTTTCGGGGCGCTGTGTACGGCTGGACCGCCGGCTCCCG 124
 QY 121 TACGAGCTGAGCCGCTTGGGGCGGGCAAGCCCTGCTAGTGTGAGACTGAAAGCAGCCG 180
 |||||||
 Db 125 TACGAGCTGAGCCGCTTGGGGCGGGCAAGCCCTGCTAGTGTGAGACTGAAAGCAGCCG 184
 QY 181 CCGGGAGCCGCGTGTGCGGGCTGTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240
 |||||||
 Db 185 CCGGGAGCCGCGTGTGCGGGCTGTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 244
 QY 241 CCGCGGGGTCTCATGTGAGAAATCCAGCTGGGCCAGAGATTTCTGCAAGCGGGAAAAATCCA 300
 |||||||
 Db 245 CCGCGGGGTCTCATGTGAGAAATCCAGCTGGGCCAGAGATTTCTGCAAGCGGGAAAAATCCA 304
 QY 301 AGGCTTATTTATGCCAGCGCTGAGTGAATTTGGCCAGTCAAGAACTTTCGCGTTAGCT 360
 |||||||
 Db 305 AGGCTTATTTATGCCAGCGCTGAGTGAATTTGGCCAGTCAAGAACTTTCGCGTTAGCT 364
 QY 361 GGCACGATATCAACTATTGGCTTGTACAGGTCTCTCAAAAATTTGSCAGAGGTGT 420
 |||||||
 Db 365 GGCACGATATCAACTATTGGCTTGTACAGGTCTCTCAAAAATTTGSCAGAGGTGT 424
 QY 421 GAGAAATCCGTATGCCCCGCTGAAATCTCGCTGACTTTGCTGTGGTGGCTTATGTGT 480
 |||||||
 Db 425 GAGAAATCCGTATGCCCCGCTGAAATCTCGCTGACTTTGCTGTGGTGGCTTATGTGT 484
 QY 481 GCACCTGGGCAATTAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGCTCAGGTCTAT 540
 |||||||
 Db 485 GCACCTGGGCAATTAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGCTCAGGTCTAT 544
 QY 541 GATCAAAATATGCTGGAAGAACAGCATATTTAAGTTCTTTCTGTGGAATAATTCAGAAA 600
 |||||||
 Db 545 GATCAAAATATGCTGGAAGAACAGCATATTTAAGTTCTTTCTGTGGAATAATTCAGAAA 604
 QY 601 TCGAGTCTGTGGAGACACCTCGAGACAGAACATGTTGGATGTGGAGCACCCTTCTAT 660
 |||||||
 Db 605 TCGAGTCTGTGGAGACACCTCGAGACAGAACATGTTGGATGTGGAGCACCCTTCTAT 664
 QY 661 AGCACTTACAGGACAGACAGATGGGGAATTCATGGCTGTGGACCAATAGAACCCCGATTG 720
 |||||||
 Db 665 AGCACTTACAGGACAGACAGATGGGGAATTCATGGCTGTGGACCAATAGAACCCCGATTG 724
 QY 721 TACGAGCTGCTGATCAAGGAGCTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
 |||||||
 Db 725 TACGAGCTGCTGATCAAGGAGCTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 784
 QY 781 ATGAGATGATTTGGCCAGAAATGAAGAAGTGTTCAGATGATTTTGCAGAAAGACAGAG 840
 |||||||
 Db 785 ATGAGATGATTTGGCCAGAAATGAAGAAGTGTTCAGATGATTTTGCAGAAAGACAGAG 844
 QY 841 GCAGATGGGTCAAAATCTTTGAGGACAGATGGCTGTGACTGCTGCGGTTGACTTTT 900
 |||||||
 Db 845 GCAGATGGGTCAAAATCTTTGAGGACAGATGGCTGTGACTGCTGCGGTTGACTTTT 904
 QY 901 GAGGAGTTGTTTCATCATGATCAACAAGAGAAAGGAGGCTCTTTATCACAGTGAAGAG 960
 |||||||
 Db 905 GAGGAGTTGTTTCATCATGATCAACAAGAGAAAGGAGGCTCTTTATCACAGTGAAGAG 964
 QY 961 CAGGAGCTGAGCCCGCCCTGCACTCTGCTTTAAACACCCAGCCATCCCTTCTTC 1020
 |||||||
 Db 965 CAGGAGCTGAGCCCGCCCTGCACTCTGCTTTAAACACCCAGCCATCCCTTCTTC 1024
 QY 1021 AAAAGGATCTTTCAATAGGAGAAACACTGAGAGATTAATTGAAGAAATTTGGATTGAGC 1080
 |||||||
 Db 1025 AAAAGGATCTTTCAATAGGAGAAACACTGAGAGATTAATTGAAGAAATTTGGATTGAGC 1084
 QY 1081 CGCGAAGAGATTTATCAGCTTAATCACTCAGATAAATCATTTGAAGATTAATAGTAAAGCT 1140
 |||||||
 Db 1085 CGCGAAGAGATTTATCAGCTTAATCACTCAGATAAATCATTTGAAGATTAATAGTAAAGCT 1144

QY 1141 AGTCTC 1146
 |||||||
 Db 1145 AGTCTC 1150
 RESULT 2
 US-09-030-607-107
 ; Sequence 107, Application US/09030607
 ; Patent No. 6262245
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
 ; NUMBER OF SEQUENCES: 224
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/030,607
 ; FILING DATE: 25-FEB-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Makl, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.427C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 107:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1621 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-09-030-607-107
 Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGCACTGAGGAGCATCTGCTGCTGAGAGCTTCGCGCCCGCCGCGCTTCTGT 60
 |||||||
 Db 5 ATGCACTGAGGAGCATCTGCTGCTGAGAGCTTCGCGCCCGCCGCGCTTCTGT 64
 QY 61 GCTATGTCCTGCTGACTTTCGGGGCGCTGTGTACGGCTGGACCGCCGGCTCCCG 120
 |||||||
 Db 65 GCTATGTCCTGCTGACTTTCGGGGCGCTGTGTACGGCTGGACCGCCGGCTCCCG 124
 QY 121 TACGAGCTGAGCCGCTTGGGGCGGGCAAGCCCTGCTAGTGTGAGACTGAAAGCAGCCG 180
 |||||||
 Db 125 TACGAGCTGAGCCGCTTGGGGCGGGCAAGCCCTGCTAGTGTGAGACTGAAAGCAGCCG 184
 QY 181 CCGGGAGCCGCGTGTGCGGGCTGTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240
 |||||||
 Db 185 CCGGGAGCCGCGTGTGCGGGCTGTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 244
 QY 241 CCGCGGGGTCTCATGTGAGAAATCCAGCTGGGCCAGAGATTTCTGCAAGCGGGAAAAATCCA 300
 |||||||
 Db 245 CCGCGGGGTCTCATGTGAGAAATCCAGCTGGGCCAGAGATTTCTGCAAGCGGGAAAAATCCA 304
 QY 301 AGGCTTATTTATGCCAGCGCTGAGTGAATTTGGCCAGTCAAGAACTTTCGCGTTAGCT 360

```

Db 305 AGGCTTATTTATCCAGAGCTGAGTGGATTGCGCAGTCAGAGACCTTCCCGTTAGCT 364
Oy 361 GGGCCACATATCAATATTTGGCTTTGTCAGTGTCTCTCAAAAATTTGCGACAGATGCT 420
Db 365 GGGCCACATATCAATATTTGGCTTTGTCAGTGTCTCTCAAAAATTTGCGACAGATGCT 424
Oy 421 GAGAAATCCGATGCCCCCGCTGATCCCTGGGTGCTTTGGTGGTGGTGGCTTATGCT 480
Db 425 GAGAAATCCGATGCCCCCGCTGATCCCTGGGTGCTTTGGTGGTGGTGGCTTATGCT 484
Oy 481 GCACCTGGGCAATTAATAGCTCTTTTTCACCGCACACACCATGCGACGGTCAGCAT 540
Db 485 GCACCTGGGCAATTAATAGCTCTTTTTCACCGCACACACCATGCGACGGTCAGCAT 544
Oy 541 GATGCAATATGCTGGGAAGAACAGCATTTAAGTCTTTTCTGTGGAAAATCTGAAA 600
Db 545 GATGCAATATGCTGGGAAGAACAGCATTTAAGTCTTTTCTGTGGAAAATCTGAAA 604
Oy 601 TCGAGTCTGTGGAGACACCTCGAGAGACAAACATGTTGGATGGTGAGCACCTTCTAT 660
Db 605 TCGAGTCTGTGGAGACACCTCGAGAGACAAACATGTTGGATGGTGAGCACCTTCTAT 664
Oy 661 ACGACTTACAGAGACAGATGGGGAATTCATGGCTGTTGGACAAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGAGACAGATGGGGAATTCATGGCTGTTGGACAAATAGAACCCAGTTC 724
Oy 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCATTCAGATGAC 780
Db 725 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCATTCAGATGAC 784
Oy 781 ATGATGATATGGCCAGAAATAGAAAGAAAGTTTGACAGATGATTTGGAAAGAACAGAG 840
Db 785 ATGATGATATGGCCAGAAATAGAAAGAAAGTTTGACAGATGATTTGGAAAGAACAGAG 844
Oy 841 GCAGAGTGTGTCAAAATCTTTGACGGACAGATGCTGTGATCCGCTTCTGACATTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGGACAGATGCTGTGATCCGCTTCTGACATTTT 904
Oy 901 GAGAGAGTGTGTATCATATCATCAAAAGAGAGCGGGCTGTTATACACATGAGAG 960
Db 905 GAGAGAGTGTGTATCATATCATCAAAAGAGAGCGGGCTGTTATACACATGAGAG 964
Oy 961 CAGAGACTGAGCCCCCGCTGACCTGCTGTTTAAACACCCAGCATCCCTTTTTC 1020
Db 965 CAGAGACTGAGCCCCCGCTGACCTGCTGTTTAAACACCCAGCATCCCTTTTTC 1024
Oy 1021 AAAAGGATCTTTTCAATAGAGAGACACACTGAGAGATCTTGAAGATTTGGATTACG 1080
Db 1025 AAAAGGATCTTTTCAATAGAGAGACACACTGAGAGATCTTGAAGATTTGGATTACG 1084
Oy 1081 CGCGAAGAGATTTATAGCTTAAGTCAATCAATCAATCAATCAATCAATCAATCAAT 1140
Db 1085 CGCGAAGAGATTTATAGCTTAAGTCAATCAATCAATCAATCAATCAATCAATCAAT 1144
Oy 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

```

```

? APPLICANT: Retter, Marc W.
? APPLICANT: Stolk, John A.
? APPLICANT: Day, Craig H.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Darrick
? APPLICANT: Li, Samuel
? APPLICANT: Wang, Aijun
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Hepler, William
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? FILE REFERENCE: 210121.427C16
? CURRENT APPLICATION NUMBER: US/09/605,785
? NUMBER OF SEQ ID NOS: 835
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 107
? LENGTH: 1621
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-605-785-107

Query Match          99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ATGGCAGTCAGAGGCACTGCTGCTGTGAGAGCTGTCCGGCTGCGCCCGGGCGTTCTGT 60
Db 5 ATGGCAGTCAGAGGCACTGCTGCTGTGAGAGCTGTCCGGCTGCGCCCGGGCGTTCTGT 64
Oy 61 GGTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 65 GGTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
Oy 121 TACGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 125 TACGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184
Oy 181 CGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 185 CGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
Oy 241 CGCGCGGTGTATGAGAAATCCACAGCTGGGCCAGAGATTTGACAGCGGGAATCCCA 300
Db 245 CGCGCGGTGTATGAGAAATCCACAGCTGGGCCAGAGATTTGACAGCGGGAATCCCA 304
Oy 301 AGGCTTATTTATGCGACAGCTGAGTGGATTGGCCAGTCAGGAACCTTCTGCGGTTAGCT 360
Db 305 AGGCTTATTTATGCGACAGCTGAGTGGATTGGCCAGTCAGGAACCTTCTGCGGTTAGCT 364
Oy 361 GGCACGATATCACTATTTTGGCTTTGTCAGGTGTTCTCTCAAAAATTTGGCAGAAGTGT 420
Db 365 GGCACGATATCACTATTTTGGCTTTGTCAGGTGTTCTCTCAAAAATTTGGCAGAAGTGT 424
Oy 421 GAGAAATCCGATGCCCCCGCTGATCCCTGGGTGCTTTGGTGGTGGTGGCTTATGCT 480
Db 425 GAGAAATCCGATGCCCCCGCTGATCCCTGGGTGCTTTGGTGGTGGTGGCTTATGCT 484
Oy 481 GCACCTGGGCAATTAATAGCTCTTTTTCACCGCACACACCATGCGACGGTCAGCAT 540
Db 485 GCACCTGGGCAATTAATAGCTCTTTTTCACCGCACACACCATGCGACGGTCAGCAT 544
Oy 541 GATGCAATATGCTGGGAAGAACAGCATTTAAGTCTTTTCTGTGGAAAATCTGAAA 600
Db 545 GATGCAATATGCTGGGAAGAACAGCATTTAAGTCTTTTCTGTGGAAAATCTGAAA 604
Oy 601 TCGAGTCTGTGGAGACACCTCGAGAGACAAACATGTTGGATGGTGAGCACCTTCTAT 660
Db 605 TCGAGTCTGTGGAGACACCTCGAGAGACAAACATGTTGGATGGTGAGCACCTTCTAT 664
Oy 661 ACGACTTACAGAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724

```

RESULT 3
US-09-605-785-107

; Sequence 107, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

[illegible]

```

QY 181 CGGGAGCCGCGCTGCTGCGGCGTCTGTGCAAGCGGTGAGTGTGCTGAGAGCCCTTC 240
    |||||
Db 185 CGGGAGCCGCGCGCTGCTGCGGCGTCTGTGCAAGCGGTGAGTGTGCTGAGAGCCCTTC 244
QY 241 CGCGGGGGTGTCAATGAGAAATCCAGCTGGGCGCAGAGTTTGTGCAAGCGGGAATCCCA 300
    |||||
Db 245 CGCGGGGGTGTCAATGAGAAATCCAGCTGGGCGCAGAGTTTGTGCAAGCGGGAATCCCA 304
QY 301 AGGCTATTATATCCAGAGCTGAGTATTTGGCCAGTCAAGAGCTTCTCCGGTATGCT 360
    |||||
Db 305 AGGCTATTATATCCAGAGCTGAGTATTTGGCCAGTCAAGAGCTTCTCCGGTATGCT 364
QY 361 GGGCAGATATCAACTATTTGGCTTGTGAGGTGTCTCAAAAATTGCGAGAGTGT 420
    |||||
Db 365 GGGCAGATATCAACTATTTGGCTTGTGAGGTGTCTCAAAAATTGCGAGAGTGT 424
QY 421 GAGATCCGATATCCCGCGCGGATTCCTGCTGAGCTTGTGCTGCTGCTGCTATGCT 480
    |||||
Db 425 GAGATCCGATATCCCGCGCGGATTCCTGCTGAGCTTGTGCTGCTGCTGCTATGCT 484
QY 481 GCACCTGGCATTTAATGAGCTTTTGTGACGCAAGCGAGCTGCAAGGGTCAAGTCTAT 540
    |||||
Db 485 GCACCTGGCATTTAATGAGCTTTTGTGACGCAAGCGAGCTGCAAGGGTCAAGTCTAT 544
QY 541 GATGCAATATGTTGGAAGAAACAGATATTTAAGTTCTTTTGTGGAAGAACTCAGAAA 600
    |||||
Db 545 GATGCAATATGTTGGAAGAAACAGATATTTAAGTTCTTTTGTGGAAGAACTCAGAAA 604
QY 601 TCGAGTCTGGAAGACACCTCGAGAGCAGATATGTTGATGTTGAGTGGAGACCTTTCTAT 660
    |||||
Db 605 TCGAGTCTGGAAGACACCTCGAGAGCAGATATGTTGATGTTGAGTGGAGACCTTTCTAT 664
QY 661 ACAGCTTACAGAGACAGACAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720
    |||||
Db 665 ACAGCTTACAGAGACAGACAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 724
QY 721 TAGAGCTGCTGATCAAAAGACTTGGACTTAATCTGATTAATCTTCCCATTCAGATGAGC 780
    |||||
Db 725 TAGAGCTGCTGATCAAAAGACTTGGACTTAATCTGATTAATCTTCCCATTCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGATTTGAGATGATTTGCAAAAGAGAGAG 840
    |||||
Db 785 ATGATGATTTGGCCAGAAATGAAGAAGATTTGAGATGATTTGCAAAAGAGAGAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGAGCGACAGATGCTGTGTGACTCGGTTGTGACTTTT 900
    |||||
Db 845 GCAGAGTGTGTCAAAATCTTTGAGCGACAGATGCTGTGTGACTCGGTTGTGACTTTT 904
QY 901 GAGAGGTTGTGATCATGATGATCAACAAGAGAGCGGGCTGTTTATCAGCAGTGAAGAG 960
    |||||
Db 905 GAGAGGTTGTGATCATGATGATCAACAAGAGAGCGGGCTGTTTATCAGCAGTGAAGAG 964
QY 961 CAGAGAGTGAAGCCCGCGCGCTGACCTGTGTAAACACCCAGCAGTCCCTTCTTC 1020
    |||||
Db 965 CAGAGAGTGAAGCCCGCGCGCTGACCTGTGTAAACACCCAGCAGTCCCTTCTTC 1024
QY 1021 AAAAGGATCTTTTATAGAGAAACACACTGAGAGATACCTTGAAGAATTTGATTCAGC 1080
    |||||
Db 1025 AAAAGGATCTTTTATAGAGAAACACACTGAGAGATACCTTGAAGAATTTGATTCAGC 1084
QY 1081 CGGGAAGATTTATACAGTTAATCAGATTAATCATTTGAAGTAAATAGGTAAGGTAAGGCT 1140
    |||||
Db 1085 CGGGAAGATTTATACAGTTAATCAGATTAATCATTTGAAGTAAATAGGTAAGGTAAGGCT 1144
QY 1141 AGTCTC 1146
    |||||
Db 1145 AGTCTC 1150

```

RESULT 7
US-09-020-956-3/c
; Sequence 3, Application US/09020956

```

; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-020-956-3

```

```

Query Match 35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 611 GGGAGAGCCTGAGGAGCAGACATGTTGATGTTGAGAGCCTTCTATACGACTTACA 670
    |||
Db 415 GGGCCCCCTCGAGGAGCAGACATGTTGATGTTGAGAGCCTTCTATACGACTTACA 356
QY 671 GGAAGAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTCTACAGCTGC 730
    |||||
Db 355 GGAAGAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTCTACAGCTGC 296
QY 731 TGATCAAGAGACTTTGAGCTTAAGTCTGATGAACCTTCCCAATCAGATGAGATGATT 790
    |||||
Db 295 TGATCAAGAGANNYGAAGTAACTCTGATGACCTTCCCAATCAGATGAGATGATT 236
QY 791 GGCAGAAATGAGAAAGAAATTTGAGATGATTTGCAAGAAGAGAGAGAGAGTGT 850
    |||||
Db 235 GGCAGAAATGAGAAAGAAATTTGAGATGATTTGCAAGAAGAGAGAGAGAGTGT 176
QY 851 GTCAAAATCTTTGAGGAGCAGATGCTGTGTGACTCCGTTTCTGACTTTTGAAGAGTTG 910
    |||||
Db 175 GTCAAAATCTTTGAGGAGCAGATGCTGTGTGACTCCGTTTCTGACTTTTGAAGAGTTG 116
QY 911 TTGATCATGATCAACAAGAGAGAGGAGCTGTTTATCACCAGTGAAGAGAGAGCTGA 970
    |||||
Db 115 TTGATCATGATCAACAAGAGAGAGGAGCTGTTTATCACCAGTGAAGAGAGAGCTGA 56
QY 971 GCGCCCGCGCTGACCTGTGCTGTAAACACCCAGCAGTCCCTTCTTCAAAAG 1025
    |||||
Db 55 GCGCCCGCGCTGACCTGTGCTGTAAACACCCAGCAGTCCCTTCTTCAAAAG 1

```

RESULT 8
US-09-030-607-3/c

```
Sequence 3, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-607-3

Query Match          35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GGGAGACCTCGAGAGACGAAGCATGTTGATGTTGGAGACACCTTCTATACGACTTACA 670
DB 415 GGGCCCCCTCGAGAGACGAAGCATGTTGATGTTGGAGACACCTTCTATACGACTTACA 356
QY 671 GGACAGCATGSGGAATTCATGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGC 730
DB 355 GGACAGCATGSGGAATTCATGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGC 296
QY 731 TGATCAAGAGACTTGACTAAAGTCTGATGAATTCCTCAATCAGATGAGCATGATGATT 790
DB 295 TGATCAAGAGANNTGACTAAAGTCTGATGAATTCCTCAATCAGATGAGCATGATGATT 236
QY 791 GGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAAAGAGAGAGAGAGAGAGTGGT 850
DB 235 GGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAAAGAGAGAGAGAGAGAGTGGT 176
QY 851 GTCAAATCTTTGACGAGCAGATGCTGTGTAAGTCCGTTCTGACTTTTGAGAGAGTTG 910
DB 175 GTCAAATCTTTGACGAGCAGATGCTGTGTAAGTCCGTTCTGACTTTTGAGAGAGTTG 116
QY 911 TTCATCATGATCAACAAGAGAGAGGCTGCTTTATCAGCAGTGGAGAGAGAGAGTGA 970
DB 115 TTCATCATGATCAACAAGAGAGAGGCTGCTTTATCAGCAGTGGAGAGAGAGTGA 56
QY 971 GCGCCGGCCCTGACCTCTGCTGTTTAAACACCCAGCATCCCTTTTCAAAAG 1025
DB 55 GCGCCGGCCCTGACCTCTGCTGTTTAAACACCCAGCATCCCTTTTCAAAAG 1
```

RESULT 9

```
US-09-605-785-3/c
Sequence 3, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harlocker, Susan L.
STREET: 11, Samuel
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/605,785
FILING DATE: 2000-06-27
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NOS: 835
SEQUENCE CHARACTERISTICS:
LENGTH: 773
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(773)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-3

Query Match          35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GGGAGACCTCGAGAGACGAAGCATGTTGATGTTGGAGACACCTTCTATACGACTTACA 670
DB 415 GGGCCCCCTCGAGAGACGAAGCATGTTGATGTTGGAGACACCTTCTATACGACTTACA 356
QY 671 GGACAGCATGSGGAATTCATGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGC 730
DB 355 GGACAGCATGSGGAATTCATGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGC 296
QY 731 TGATCAAGAGACTTGACTAAAGTCTGATGAATTCCTCAATCAGATGAGCATGATGATT 790
DB 295 TGATCAAGAGANNTGACTAAAGTCTGATGAATTCCTCAATCAGATGAGCATGATGATT 236
QY 791 GGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAAAGAGAGAGAGAGAGAGTGGT 850
DB 235 GGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAAAGAGAGAGAGAGAGAGTGGT 176
QY 851 GTCAAATCTTTGACGAGCAGATGCTGTGTAAGTCCGTTCTGACTTTTGAGAGAGTTG 910
DB 175 GTCAAATCTTTGACGAGCAGATGCTGTGTAAGTCCGTTCTGACTTTTGAGAGAGTTG 116
QY 911 TTCATCATGATCAACAAGAGAGAGGCTGCTTTATCAGCAGTGGAGAGAGAGAGTGA 970
DB 115 TTCATCATGATCAACAAGAGAGAGGCTGCTTTATCAGCAGTGGAGAGAGAGTGA 56
QY 971 GCGCCGGCCCTGACCTCTGCTGTTTAAACACCCAGCATCCCTTTTCAAAAG 1025
DB 55 GCGCCGGCCCTGACCTCTGCTGTTTAAACACCCAGCATCCCTTTTCAAAAG 1
```

RESULT 10
US-09-439-313-3/c

```
; Sequence 3, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-3
```

```
Query Match 35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 611 GGGAGACCTCGAGCAGACACATGTTGGATGAGAGACCTTTCTATACGACTTACA 670
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 415 GGGCCCCCTCGAGCAGACACATGTTGGATGAGAGACCTTTCTATACGACTTACA 356
QY 671 GGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTCTAGAGCTGC 730
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 355 GGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTCTAGAGCTGC 296
QY 731 TGATCAAGAGACTTGCACTAAAGTCTGATGACCTCCCAATCAGATGAGATGATTT 790
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 295 TGATCAAGAGANNMGACTAAAGTCTGATGACCTCCCAATCAGATGAGATGATTT 236
QY 791 GGCCAGAAATGAGAGAAAGATTGACAGATATTTGCAAAAGAGAGAGAGAGAGTGT 850
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 235 GGCCAGAAATGAGAGAAAGATTGACAGATATTTGCAAAAGAGAGAGAGAGTGT 176
QY 851 GTCAAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTTGAGAGAGTGT 910
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 175 GTCAAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTTGAGAGAGTGT 116
QY 911 TTCATCATGATCAACAAGAGAGAGGGGCTGTTTATCACAGTAGAGAGAGAGCTGA 970
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 115 TTCATCATGATCAACAAGAGAGAGGGGCTGTTTATCACAGTAGAGAGAGAGCTGA 56
QY 971 GCGCCCGCCCTGCACTCTGCTGTTAAACGCCAGCATCCCTCTTTCAAAAG 1025
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 55 GCGCCCGCCCTGCACTCTGCTGTTAAACGCCAGCATCCCTCTTTCAAAAG 1
```

```
RESULT 11
US-09-352-616A-3/C
; Sequence 3, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
```

```
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-3
```

```
Query Match 35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 611 GGGAGACCTCGAGCAGACACATGTTGGATGAGAGACCTTTCTATACGACTTACA 670
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 415 GGGCCCCCTCGAGCAGACACATGTTGGATGAGAGACCTTTCTATACGACTTACA 356
QY 671 GGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTCTAGAGCTGC 730
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 355 GGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTCTAGAGCTGC 296
QY 731 TGATCAAGAGACTTGCACTAAAGTCTGATGACCTCCCAATCAGATGAGATGATTT 790
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 295 TGATCAAGAGANNMGACTAAAGTCTGATGACCTCCCAATCAGATGAGATGATTT 236
QY 791 GGCCAGAAATGAGAGAAAGATTGACAGATATTTGCAAAAGAGAGAGAGAGTGT 850
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 235 GGCCAGAAATGAGAGAAAGATTGACAGATATTTGCAAAAGAGAGAGAGAGTGT 176
QY 851 GTCAAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTTGAGAGAGTGT 910
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 175 GTCAAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCTGACTTTTGAGAGAGTGT 116
QY 911 TTCATCATGATCAACAAGAGAGAGGGGCTGTTTATCACAGTAGAGAGAGAGCTGA 970
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 115 TTCATCATGATCAACAAGAGAGAGGGGCTGTTTATCACAGTAGAGAGAGAGCTGA 56
QY 971 GCGCCCGCCCTGCACTCTGCTGTTAAACGCCAGCATCCCTCTTTCAAAAG 1025
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 55 GCGCCCGCCCTGCACTCTGCTGTTAAACGCCAGCATCCCTCTTTCAAAAG 1
```

```
RESULT 12
US-09-232-149A-3/C
; Sequence 3, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
```


PI Richardson J, Monahan J;
 XX WPI; 2002-405070/43.
 DR P-PSDB; AAE23971.
 XX
 PT Determining risk for prostate cancer in subject or risk for metastatic
 PT prostate cancer to liver or lymph nodes of prostate cancer patients,
 PT comprises measuring expression or activity of alpha-methylacyl-CoA
 PT racemase -
 XX
 PS Claim 54; Fig 1; 102pp; English.
 XX
 CC The present invention relates to novel methods for determining whether
 CC an individual is at risk for prostate cancer or whether a prostate cancer
 CC patient is at risk for metastatic prostate cancer to the liver or lymph
 CC nodes. The method involves measuring the expression or activity of
 CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
 CC in diagnostic methods, drug screening assays, and in treating or
 CC preventing cancer, e.g. prostate cancer. The present sequence is human
 CC alpha-methyl-acyl-CoA racemase SV1 cDNA.
 CC
 XX Sequence 2005 BP; 519 A; 427 C; 514 G; 545 T; 0 other;
 XX
 Query Match 100.0%; Score 1146; DB 24; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACTGCAAGGCACTCTGCTGAGCTGCCGCTGCGCCGCGCGCTTCGT 60
 DB 66 ATGCACTGCAAGGCACTCTGCTGAGCTGCCGCTGCGCCGCGCTTCGT 125
 QY 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 126 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
 QY 121 TAGACGCTGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 DB 186 TAGACGCTGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245
 QY 181 CGGCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 246 CGGCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
 QY 241 CGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 306 CGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
 QY 301 AGGCTTATTTATGCGAGCGCTGAGTGATTTGGCCAGTCAAGAACCTTCTGCGGTTAGCT 360
 DB 366 AGGCTTATTTATGCGAGCGCTGAGTGATTTGGCCAGTCAAGAACCTTCTGCGGTTAGCT 425
 QY 361 GGCACAGATATCAACTATTTGGCTTTTGCAGAGTCTCTCAAAATTTGGCAGAAGTGT 420
 DB 426 GGCACAGATATCAACTATTTGGCTTTTGCAGAGTCTCTCAAAATTTGGCAGAAGTGT 485
 QY 421 GAGAAATCCGATGCGCGCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 486 GAGAAATCCGATGCGCGCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 545
 QY 481 GCACTGGGCAATTATAGGCGCTTTTGGACGCGACAGCACTGGCAAGGCTCAGTAT 540
 DB 546 GCACTGGGCAATTATAGGCGCTTTTGGACGCGACAGCACTGGCAAGGCTCAGTAT 605
 QY 541 GATGCAATATGCTGAGAGGAAAGCATATTTAAGTCTTTTCTGCGAAATCTCAGAA 600
 DB 606 GATGCAATATGCTGAGAGGAAAGCATATTTAAGTCTTTTCTGCGAAATCTCAGAA 665
 QY 601 TCGAGTCTGTTGGAGAGCACTCGAGGACAGAACTGTTGATGCTGAGACCTTTCTAT 660
 DB 666 TCGAGTCTGTTGGAGAGCACTCGAGGACAGAACTGTTGATGCTGAGACCTTTCTAT 725
 QY 661 ACGCTTACGAGGAGAGGAGATGCGGGAATTCATGCTGTTGAGCAATAGAACCCACGTC 720
 DB 726 ACGCTTACGAGGAGAGGAGATGCGGGAATTCATGCTGTTGAGCAATAGAACCCACGTC 785

DB 726 ACGCTTACGAGGAGAGGAGATGCGGGAATTCATGCTGTTGAGCAATAGAACCCACGTC 785
 QY 721 TAGAGCTGCTGATCAAAAGGACTTGAATGAATCTGATGAACTTCCCAATCAGATGAGC 780
 DB 786 TAGAGCTGCTGATCAAAAGGACTTGAATGAATCTGATGAACTTCCCAATCAGATGAGC 845
 QY 781 ATGATGATTTGGCCAGAAATGAGAGAGTTTCCAGATGATTTGCAAAAGACGAG 840
 DB 846 ATGATGATTTGGCCAGAAATGAGAGAGTTTCCAGATGATTTGCAAAAGACGAG 905
 QY 841 GCAGAGTGTGTCAAATCTTTGAGCGGACAGATGCTGTGTGACTCCGGTCTGACTTTT 900
 DB 906 GCAGAGTGTGTCAAATCTTTGAGCGGACAGATGCTGTGTGACTCCGGTCTGACTTTT 965
 QY 901 GAGAGGTTGCTCATCATGATCACAGAGGAGGAGGCTGTTATACCAAGTGAAGAG 960
 DB 966 GAGAGGTTGCTCATCATGATCACAGAGGAGGAGGCTGTTATACCAAGTGAAGAG 1025
 QY 961 CAGAGCTGAGCGCGCGCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTTTC 1020
 DB 1026 CAGAGCTGAGCGCGCGCGCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTTTC 1085
 QY 1021 AAAGGGATCTTTCATAGGAGACACAGTGAAGATCTTGAAGATTTGATGAGC 1080
 DB 1086 AAAGGGATCTTTCATAGGAGACACAGTGAAGATCTTGAAGATTTGATGAGC 1145
 QY 1081 CGCGAAGAGATTTATCAGCTTAATCAATCAATTTGAAGATTTGAAGATTTGAAGAT 1140
 DB 1146 CGCGAAGAGATTTATCAGCTTAATCAATCAATTTGAAGATTTGAAGATTTGAAGAT 1205
 QY 1141 AGTCTC 1146
 DB 1206 AGTCTC 1211

RESULT 2
 AAD38607
 ID AAD38607 standard; cDNA; 2005 BP.
 AC AAD38607;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human alpha-methylacyl-CoA racemase splice variant, SV4 cDNA.
 XX
 KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
 KW cytosolic; SV4; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 66..1214
 FT /*lag- a
 FT /product= "Human SV4 protein"
 XX
 FN W0200227324-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 28-SEP-2001; 2001WO-US30532.
 XX
 PR 28-SEP-2000; 2000US-236238P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Richardson J, Monahan J;
 XX WPI; 2002-405070/43.
 DR P-PSDB; AAE23971.
 XX
 PT Determining risk for prostate cancer in subject or risk for metastatic
 PT prostate cancer to liver or lymph nodes of prostate cancer patients,
 PT comprises measuring expression or activity of alpha-methylacyl-CoA

PT racemase -
 XX Claim 54: Fig 9; 102pp; English.
 PS
 CC The present invention relates to novel methods for determining whether
 CC an individual is at risk for prostate cancer or whether a prostate cancer
 CC patient is at risk for metastatic prostate cancer to the liver or lymph
 CC nodes. The method involves measuring the expression or activity of
 CC alpha-methylacyl-CoA racemase. Sequences of the invention or activity of
 CC in diagnostic methods, drug screening assays, and in treating or
 CC preventing cancer, e.g., prostate cancer. The present sequence is human
 CC alpha-methyl-acyl-CoA racemase splice variant, SV4 cDNA.
 XX
 SQ Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 other:
 Query Match 100.0%; Score 1146; DB 24; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGGCACTGCAAGGCACTCGGTGCTGGAAGCTCGGGCCCTGGCCCGGCGCTTCTGT 60
 66 ATGGCACTGCAAGGCACTCGGTGCTGGAAGCTCGGGCCCTGGCCCGGCGCTTCTGT 125
 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 126 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
 121 TACGACGTAGCCGCTTGGCGCGGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 186 TACGACGTAGCCGCTTGGCGCGGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
 181 CGGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 246 CGGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
 241 CGGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 306 CGGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
 301 AGGCTTATTTATGCAAGGCACTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 366 AGGCTTATTTATGCAAGGCACTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
 361 GGGCAGATATCACTATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 426 GGGCAGATATCACTATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
 421 GAGAAATCCCTATGCCCCCTGTAATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 486 GAGAAATCCCTATGCCCCCTGTAATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
 481 GCACTGGCATATATGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 546 GCACTGGCATATATGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
 541 GATGCAAAATATGCTGGAAGAAAGCATATTTAAGTCTTTCTGGAAGAAATCAAGAA 600
 606 GATGCAAAATATGCTGGAAGAAAGCATATTTAAGTCTTTCTGGAAGAAATCAAGAA 665
 601 TCGAGCTGCTGGAAGCACTCGAGACACACATGTTGGATGCTGGAAGCACTTTCTAT 660
 666 TCGAGCTGCTGGAAGCACTCGAGACACACATGTTGGATGCTGGAAGCACTTTCTAT 725
 661 AGCACTTACGACAGACAGATGGAATTCATGCTGTTGGAGCAATAGAAACCCCAAGTTC 720
 726 ACAGCTTACGACAGACAGATGGAATTCATGCTGTTGGAGCAATAGAAACCCCAAGTTC 785
 721 TACGACCTCTGATCAAGAGACTTGACTGAATCTGATGAATCTCCCAATCAGATGAGC 780
 786 TACGACCTCTGATCAAGAGACTTGACTGAATCTGATGAATCTCCCAATCAGATGAGC 845
 781 ATGATGATGCTGCGCAAGAAATGAAGAAAGTTGACATGATGTTTGGCAAGAGACGAG 840

Db 846 ATGATGATGCTGCGCAAGAAATGAGAGAAAGTTTGCAGATGATATTTGCCAAGAGCAGAG 905
 841 GCAGAGTGTGTCAAATCTTTGACGGCACAGATCCCTGCTGACTCGGTTCTGACTTTT 900
 906 GCAGAGTGTGTCAAATCTTTGACGGCACAGATCCCTGCTGACTCGGTTCTGACTTTT 965
 901 GAGAGAGTTGTCATCATGATGATCACAACAGAGAGGGGCTCGTTTATCAGCAGTGAAG 960
 966 GAGAGAGTTGTCATCATGATGATCACAACAGAGAGGGGCTCGTTTATCAGCAGTGAAG 1025
 961 CAGAGAGTGAAGCCCGCCGCTGACACTGCTGCTGTTAAACCCGACACCTGCTTTC 1020
 1026 CAGAGAGTGAAGCCCGCCGCTGACACTGCTGCTGTTAAACCCGACACCTGCTTTC 1085
 1021 AAAAGGATCTTTTATCAGATGAGACACACTGAGAGATCTTGAAGATTTGATTCAGC 1080
 1086 AAAAGGATCTTTTATCAGATGAGACACACTGAGAGATCTTGAAGATTTGATTCAGC 1145
 1081 CCGGAAGATTTTATCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1140
 1146 CCGGAAGATTTTATCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1205
 1141 AGTCTC 1146
 1206 AGTCTC 1211
 Db
 RESULT 3
 AAD38604
 ID AAD38604 standard; cDNA; 2069 BP.
 XX
 AC AAD38604;
 XX
 DT 23-SEP-2002 (first entry)
 DE
 XX Human alpha-methylacyl-CoA racemase SV1 cDNA #2.
 XX
 KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
 KW Cytosolic; SV1; gene; ss.
 OS
 XX Homo sapiens.
 FH
 FX Key Location/Qualifiers
 FT 90..1238
 FT CDS /*tag=a
 FT /product="Human SV1 protein #2"
 XX
 PN WO200227324-A2.
 PD
 PD 04-APR-2002.
 XX
 PF 28-SEP-2001; 2001WO-US30532.
 PF
 PR 28-SEP-2000; 2000US-236238P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Richardson J, Monahan J;
 FI
 FI WPI: 2002-405070/43.
 DR
 DR P-PSDB: AAE23972.
 XX
 PT Determining risk for prostate cancer in subject or risk for metastatic
 PT prostate cancer to liver or lymph nodes of prostate cancer patients,
 PT comprises measuring expression or activity of alpha-methylacyl-CoA
 PT racemase -
 XX
 PS Claim 54: Fig 3; 102pp; English.
 CC The present invention relates to novel methods for determining whether
 CC an individual is at risk for prostate cancer or whether a prostate cancer
 CC patient is at risk for metastatic prostate cancer to the liver or lymph
 CC nodes. The method involves measuring the expression or activity of

CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful in diagnostic methods, drug screening assays, and in treating or preventing cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-acyl-CoA racemase SV1 cDNA.

XX Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGGCACTGAGGCGCATCTGCTGCTGAGCTTCGCGCTGGCCCGCCGCTTCTGT 60
DB 90 ATGGCACTGAGGCGCATCTGCTGCTGAGCTTCGCGCTGGCCCGCCGCTTCTGT 149
QY 61 GCTATGGTCTGGCTGACTCGGGGGCGGCTGTACGGCTGGACCGGCGCCGCTCCG 120
DB 150 GCTATGGTCTGGCTGACTCGGGGGCGGCTGTACGGCTGGACCGGCGCCGCTCCG 209
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGCTGAGCAAGCAAGCCG 180
DB 210 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGCTGAGCAAGCAAGCCG 269
QY 181 CGGGAGACCCGCTGCTGCGGCGCTGTGTGCAACGGTGGATGCTGCTGAGACCTTC 240
DB 270 CGGGAGACCCGCTGCTGCGGCGCTGTGTGCAACGGTGGATGCTGCTGAGACCTTC 329
QY 241 CGCGCGGCTGCAATGAGAACTCCAGCTGGGCGGCAAGATTCGACGCGGAAATCCA 300
DB 330 CGCGCGGCTGCAATGAGAACTCCAGCTGGGCGGCAAGATTCGACGCGGAAATCCA 389
QY 301 AGGCTTATTTATGCGCAGCTGAGTGATTTGGCCAGTCAAGAAAGCTTCCGCGTTAGCT 360
DB 390 AGGCTTATTTATGCGCAGCTGAGTGATTTGGCCAGTCAAGAAAGCTTCCGCGTTAGCT 449
QY 361 GGGCAGATATCAATTTGGCTTGTGCTGAGTGTCTCAAAAATTTGGCAGAAAGTGT 420
DB 450 GGGCAGATATCAATTTGGCTTGTGCTGAGTGTCTCAAAAATTTGGCAGAAAGTGT 509
QY 421 GAGAAATCCGTAATCCCGCGTGAATCTCCGCTGACTTTGCTGGTGGCTTATGT 480
DB 510 GAGAAATCCGTAATCCCGCGTGAATCTCCGCTGACTTTGCTGGTGGCTTATGT 569
QY 481 GCACTGGGCAATTAATGCTCTTTTGGACCGACACGCACTGGCAAGGTCAAGTCAAT 540
DB 570 GCACTGGGCAATTAATGCTCTTTTGGACCGACACGCACTGGCAAGGTCAAGTCAAT 629
QY 541 GATGCAAAATATGTTGGAAGGACAGCATATTTAAGTCTTTCTGTGGAATAACACGAA 600
DB 630 GATGCAAAATATGTTGGAAGGACAGCATATTTAAGTCTTTCTGTGGAATAACACGAA 689
QY 601 TCGAGTCTGTGGAGACGACCTCGAGACAGAACATGTTGATGGTGGAGACCTTTCTAT 660
DB 690 TCGAGTCTGTGGAGACGACCTCGAGACAGAACATGTTGATGGTGGAGACCTTTCTAT 749
QY 661 AGCACTTACAGACAGACAGATGGGAATTCATGCTGTTGGACCAATAGAACCCCAATTC 720
DB 750 AGCACTTACAGACAGACAGATGGGAATTCATGCTGTTGGACCAATAGAACCCCAATTC 809
QY 721 TAGAGCTGTGTGCAAAAGGACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
DB 810 TAGAGCTGTGTGCAAAAGGACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 869
QY 781 ATGATGATATGGCCAGAAATGAGAAAGAAATTTGAGATATTTTGGCAAGAGACGAG 840
DB 870 ATGATGATATGGCCAGAAATGAGAAAGAAATTTGAGATATTTTGGCAAGAGACGAG 929
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGCTTCTGACTTTT 900
DB 930 GCAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGCTTCTGACTTTT 989
QY 901 GAGAGGTGTGTATCATGATGACAAACAGAGAGGCGCTGTTTATCACCAGTGAAGAG 960

```

```

DB 990 GAGAGGTGTGTATCATGATGACAAACAGAGAGGCGCTGTTTATCACCAGTGAAGAG 1049
QY 961 CAGAGCTGAGACCCCGCCGCTGACCTGTGCTGTTTAAACACCCAGCATCCCTTCTTC 1020
DB 1050 CAGAGCTGAGACCCCGCCGCTGACCTGTGCTGTTTAAACACCCAGCATCCCTTCTTC 1109
QY 1021 AAAAGGATCCCTTTCATAGAGAAACACTGAGAGATACCTGAGAAATTTGGATTCAGC 1080
DB 1110 AAAAGGATCCCTTTCATAGAGAAACACTGAGAGATACCTGAGAAATTTGGATTCAGC 1169
QY 1081 CGGAGAGATTTATACGCTTAACTCAGATAAATATGAAATGAAATGAAAGCT 1140
DB 1170 CGGAGAGATTTATACGCTTAACTCAGATAAATATGAAATGAAATGAAAGCT 1229
QY 1141 AGTCTC 1146
DB 1230 AGTCTC 1235

RESULT 4
AAV61199
ID AAV61199 standard; cDNA; 1621 BP.
XX
AC AAV61199;
XX
XT 06-JAN-1999 (first entry)
XX
DE Full length cDNA sequence of prostate tumour clone F1-12.
XX
KM Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN M09837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03492.
XX
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillion DC, Xu J;
XX
DR WPI: 1998-609886/51.
DR P-PSDB; AAW71867.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 76-77; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 19; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGAGGCGCATCTGCTGCTGAGCTTCGCGCTGGCCCGCCGCTTCTGT 60
DB 5 ATGGCACTGAGGCGCATCTGCTGCTGAGCTTCGCGCTGGCCCGCCGCTTCTGT 64
QY 61 GCTATGGTCTGGCTGACTCGGGGGCGGCTGTACGGCTGGACCGGCGCCGCTCCGCG 120

```

Db	65	GCATATGCTCTTGCGCATCTTCCTGGGGGGCGCTGTGTACCGCTGTGGACCGGGCCGGCTCCGC	124
Qy	121	TACGACGTAGCCGCTTGTGGCCGGGGCAAGCCCTCGTAGTGCCTGGACCCGMAAGACGCG	180
Db	125	TACGACGTAGCCGCTTGTGGCCGGGGCAAGCCCTCGTAGTGCCTGGACCCGMAAGACGCG	184
Qy	181	CGGGAGCCGCGCTGTGCTGGCCGCTGTGTCAAGCGGTGGATGGCTGGCGTGGAGCCCTTC	240
Db	185	CGGGAGCCGCGCTGTGCTGGCCGCTGTGTCAAGCGGTGGATGGCTGGCGTGGAGCCCTTC	244
Qy	241	CGCGGGGTGTATGATGGAGAAATCCGAGCTGGGGCCGAGAAATCTCGACGGGGAAATCCA	300
Db	245	CGCGGGGTGTATGATGGAGAAATCCGAGCTGGGGCCGAGAAATCTCGACGGGGAAATCCA	304
Qy	301	AGGCTATTTTATGACAGCGAGTGGATTTTGGCCAGTCAGAGAAAGCTTTCGCGGTAACT	360
Db	305	AGGCTATTTTATGACAGCGAGTGGATTTTGGCCAGTCAGAGAAAGCTTTCGCGGTAACT	364
Qy	361	GGCGACGATATCACATTTTGGCTTTGTGAGGTGTCTCCAAAAATTTGGCAGAAAGTGT	420
Db	365	GGCGACGATATCACATTTTGGCTTTGTGAGGTGTCTCCAAAAATTTGGCAGAAAGTGT	424
Qy	421	GAGAAATCCGTATGCCCCGCTGAAATCTCTGGCTACATTTGCTGGTGGCCCTTATGTGT	480
Db	425	GAGAAATCCGTATGCCCCGCTGAAATCTCTGGCTACATTTGCTGGTGGCCCTTATGTGT	484
Qy	481	GCAGTGGGCATTTAATATGCTCTTTTATACGCGACACGACGCGCAAGGGTCAGGTATTT	540
Db	485	GCAGTGGGCATTTAATATGCTCTTTTATACGCGACACGACGCGCAAGGGTCAGGTATTT	544
Qy	541	GATGCAATATATGGGAGAGAACACACATATTTAAAGTTCTTTCTGTGGAAAACTCAGAAA	600
Db	545	GATGCAATATATGGGAGAGAACACACATATTTAAAGTTCTTTCTGTGGAAAACTCAGAAA	604
Qy	601	TCGATCTGGGGGAAGACACTCTGGAGAGACAGAAATCTGTGGATGTGGAGCACCTTTCTAT	660
Db	605	TCGATCTGGGGGAAGACACTCTGGAGAGACAGAAATCTGTGGATGTGGAGCACCTTTCTAT	664
Qy	661	ACGACTTACAGGACAGCAGATATGGGAATTCATGCTGTGGAGCAATAGAAACCCCAAGTTC	720
Db	665	ACGACTTACAGGACAGCAGATATGGGAATTCATGCTGTGGAGCAATAGAAACCCCAAGTTC	724
Qy	721	TACGACGTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATCTTCCATTCAGATAGAC	780
Db	725	TACGACGTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATCTTCCATTCAGATAGAC	784
Qy	781	ATGATGATTTGGCCAGAAATGAAGAAACAACTTTGCAAGATGTATTGGCAAAAGAGACGAG	840
Db	785	ATGATGATTTGGCCAGAAATGAAGAAACAACTTTGCAAGATGTATTGGCAAAAGAGACGAG	844
Qy	841	GCAGAGTGTCTCAATCTTTGAGCGACAGATGCGCTGTGGACCCGGTTCGACTTGT	900
Db	845	GCAGAGTGTCTCAATCTTTGAGCGACAGATGCGCTGTGGACCCGGTTCGACTTGT	904
Qy	901	GAGAGAGTTGTTCATCATGATCACAAACAGAGAAACGGGGCTCGTTTATCACACGTAGAG	960
Db	905	GAGAGAGTTGTTCATCATGATCACAAACAGAGAAACGGGGCTCGTTTATCACACGTAGAG	964
Qy	961	CAGAGGTAGAGCCCCCGCCCGACACCTGTGCTTTAAACACCCACGCAATCCCTTCTTTC	1020
Db	965	CAGAGGTAGAGCCCCCGCCCGACACCTGTGCTTTAAACACCCACGCAATCCCTTCTTTC	1024
Qy	1021	AAAAAGGATCTTTTATATGAGAAACACACTGAGAGAGATCTTGAAGAAATTTGGATTACG	1080
Db	1025	AAAAAGGATCTTTTATATGAGAAACACACTGAGAGAGATCTTGAAGAAATTTGGATTACG	1084
Qy	1081	CGCGAAGAGATTTATACGCTTAACTCAGATTAATAAATCATTTGAAGTAATTAAGGTAAACCT	1140
Db	1085	CGCGAAGAGATTTATACGCTTAACTCAGATTAATAAATCATTTGAAGTAATTAAGGTAAACCT	1144
Qy	1141	AGTCTC 1146	

Db 1145 AGTCCTC 1150

RESULT 5
ID AAV58584 standard; cDNA; 1621 BP.
AAV58584;
08-DEC-1998 (first entry)
Prostate tumour specific gene clone Fl-12.
Prostate tumour specific gene; human; prostate cancer; detection;
therapy; ss.
Homo sapiens.

Key Location/Qualifiers
FT CDS 5..1153
FT CDS /*tag= a

WO9837418-A2.
27-AUG-1998.
25-FEB-1998; 98MO-US03690.
09-FEB-1998; 98US-0904809.
25-FEB-1997; 97US-0805396.
21-AUG-1997; 97US-0904809.
(CORI-) CORIXA CORP.
Dillon DC, Xu J;
WPI: 1998-480805/41.
F-PSDB: AAM69383.

Novel human prostate specific tumour protein and fragments - useful
for detecting and treating prostate cancers

Claim 1; Page 81-82; 141pp; English.

This sequence represents a human prostate tumour specific gene, and can
be used in the method of the invention. The method is for detecting
prostate cancer comprises contacting a biological sample with an agent
able to bind an immunogenic portion of a prostate protein (such as
encoded by this sequence). An antibody which binds to an immunogenic
portion of the prostate protein, and the method can be used to detect,
monitor progression of, or treat prostate cancers. The antibody may
also be conjugated to a therapeutic agent for use in therapy of prostate
cancers.

Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other:

Query Match 99.7%; Score 1142.8; DB 19; Length 1621;
Best Local Similarity 99.8%; Pred No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

1 ATGGGACCTGACGAGCTGCTGGGCTGGGAGCTGTCCGGCTGCGGCGCCGCTTCTGT 60
5 ATGGGACCTGACGAGCTGCTGGGCTGGGAGCTGTCCGGCTGCGGCGCCGCTTCTGT 60
61 GGTATGCTGCTGGGCTGCTGGGCTGGGAGCTGTCCGGCTGCGGCGCCGCTTCTGT 120
65 GGTATGCTGCTGGGCTGCTGGGCTGGGAGCTGTCCGGCTGCGGCGCCGCTTCTGT 124
121 TACGAGCTGAGCCCTTGGGCGGGGCAAGCGCTTGTAGTGTGGAGCTGAACAGACCG 180
125 TACGAGCTGAGCCCTTGGGCGGGGCAAGCGCTTGTAGTGTGGAGCTGAACAGACCG 184
181 CGGGAGCGCCGCTGCTGCGGCTGTGTGCAAGCGCTGCGGATGTGCTGTGAGCCCTTG 240

|||||
Db 185 CGGGAGCCGCTGCTGCGGCGCTGCTGCAAGGCGTCGATGCTGCTGGAGCCCTTC 244
QY 241 CGCGCGGCTGTCAGGAACCTCCAGCTGGCCAGAGATTCGACCGGGAATCA 300
Db 245 CGCGCGGCTGTCAGGAACCTCCAGCTGGCCAGAGATTCGACCGGGAATCA 304
QY 301 AGGCTTATTTATGCCAGGCTAGTGATTTTGGCCAGAGAACTTTCGCGGTAGCT 360
Db 305 AGGCTTATTTATGCCAGGCTAGTGATTTTGGCCAGAGAACTTTCGCGGTAGCT 364
QY 361 GCGCAGCATATCACTATTTGGCTTTGTCAGAGTCTCTCTAAAAATTTGGCAGAGTGT 420
Db 365 GGCACAGATATCACTATTTGGCTTTGTCAGAGTCTCTCTAAAAATTTGGCAGAGTGT 424
QY 421 GAGATCCGATATGCCCGCTGATCTCTGCTGCTGATTTGCTGGGCTTATGCT 480
Db 425 GAGATCCGATATGCCCGCTGATCTCTGCTGCTGATTTGCTGGGCTTATGCT 484
QY 481 GCACTGGGCAATTAATGCTCTTTTGGACCGCACACGCACTGGCAGAGTCAAT 540
Db 485 GCACTGGGCAATTAATGCTCTTTTGGACCGCACACGCACTGGCAGAGTCAAT 544
QY 541 GATCAATATGCTGGAAGGACAGCAATATTTAGTCTTTTCTGTGAAAACTCAGAA 600
Db 545 GATCAATATGCTGGAAGGACAGCAATATTTAGTCTTTTCTGTGAAAACTCAGAA 604
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGCAATGTTGATGGTGGAGCACTTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACTCGAGGACAGCAATGTTGATGGTGGAGCACTTTCTAT 664
QY 661 ACGACTTACAGAGACAGCATGAGGGAATTCATGCTGTGGAGCANTGAACCCAGTTC 720
Db 665 ACGACTTACAGAGACAGCATGAGGGAATTCATGCTGTGGAGCANTGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGCACTTGGATTAAGTCTGATGAATTCCTCAATCAGATGAC 780
Db 725 TACGAGCTGCTGATCAAAAGCACTTGGATTAAGTCTGATGAATTCCTCAATCAGATGAC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCAAAAGACGAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCAAAAGACGAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGAGGCGCAGATGCTGTGACCTCCGTTCTGACTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGAGGCGCAGATGCTGTGACCTCCGTTCTGACTTT 904
QY 901 GAGGAGTGTGTCAATCATGATCACAACAAGGAGCGGCTGTTTATACAGTGAAGAG 960
Db 905 GAGGAGTGTGTCAATCATGATCACAACAAGGAGCGGCTGTTTATACAGTGAAGAG 964
QY 961 CAGGACGTGAGCCCGCCCTGCACTCTGCTGTTTAAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGGACGTGAGCCCGCCCTGCACTCTGCTGTTTAAACACCCAGCCATCCCTTCTTC 1024
QY 1021 AAAAGGATCTTTTCATATGGAACACACTGAGAGATCTTGAAGATTTGGATTCAGC 1080
Db 1025 AAAAGGATCTTTTCATATGGAACACACTGAGAGATCTTGAAGATTTGGATTCAGC 1084
QY 1081 CGCGAAGGATTTATCAGCTTAATCAGATTAATTAATCATTTGAAGATTAAGTAAACCT 1140
Db 1085 CGCGAAGGATTTATCAGCTTAATCAGATTAATTAATCATTTGAAGATTAAGTAAACCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 6
ID AAA06347
XX AAA06347 standard; cdna; 1621 BP.
AC AAA06347;

XX 13-JUN-2000 (first entry)
XX Human immunogenic prostate tumour protein cdna sequence SEQ ID NO:107.
DE Human: prostate cancer; diagnosis; tumour; gene therapy; detection;
KW Immunogenic; cytosolic; vaccine; ss.
OS Homo sapiens.
XX WO200004149-A2.
PN 27-JAN-2000.
PD 14-JUL-1999; 99WO-US15838.
PF 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX (COR-) CORIXA CORP.
XX Dillion DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
PI WPI; 2000-171268/15.
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
PS Claim 1; Page 133-134; 263pp; English.
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (pmp). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA0691 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention.
XX Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
SQ
Query Match 99.7%; Score 1142.8; DB 21; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
QY 1 ATGCACTGCAAGGACATCTCGCTGAGCTGCCGCTCGCCCGGCGCTTCTGT 60
Db 5 ATGCACTGCAAGGACATCTCGCTGAGCTGCCGCTCGCCCGGCGCTTCTGT 64
QY 61 GCTATGCTCGCTGAGCTTGGGCGGCTGTGTAGCGCGGACCGGCGGCTCCCGC 120
Db 65 GCTATGCTCGCTGAGCTTGGGCGGCTGTGTAGCGCGGACCGGCGGCTCCCGC 124
QY 121 TACGACGTGAGCCCGCTTGGGCGGAGGCTCGCTAGTGTGAGCATGAACAGCGC 180
Db 125 TACGACGTGAGCCCGCTTGGGCGGAGGCTCGCTAGTGTGAGCATGAACAGCGC 184
QY 181 CGGGAGCGCGCTGTGCGGCGCTGTGCAAGCGGTGAGTGTGCTGAGACCGT 188
Db 185 CGGGAGCGCGCTGTGCGGCGCTGTGCAAGCGGTGAGTGTGCTGAGACCGT 192
QY 241 CGCGCGGCTGTCATGGAACCTCCAGCTGGGCCCAAGATTTCTGACGCGG 244

```

Db 245 CGCGCGGTGTCATGAGAAACTCCAGCTGGGCCAGAGATTCTGACGGGAAATCCA 304
QY 301 AGGCTATTATTCAGAGCTGAGTGATTTGGCCATCGAGAAAGCTTCTGGCGTACGT 360
Db 305 AGGCTATTATTCAGAGCTGAGTGATTTGGCCATCGAGAAAGCTTCTGGCGTACGT 364
QY 361 GGGCAGATATCACTATTGCTTGGCTTGTGAGTGTCTCTCAAAAATTTGCCAGAGTGT 420
Db 365 GGGCAGATATCACTATTGCTTGGCTTGTGAGTGTCTCTCAAAAATTTGGAGAGTGT 424
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGTGTGGCTTATGT 480
Db 425 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGTGTGGCTTATGT 484
QY 481 GCACTGGCATTTATATGCTCTTTTGTGACCGACAGCACTGGCAAGGTCAGTCAAT 540
Db 485 GCACTGGCATTTATATGCTCTTTTGTGACCGACAGCACTGGCAAGGTCAGTCAAT 544
QY 541 GATGCAAAATATGTTGTAAGAGAAAGCAATTTTAAAGTCTTTTCTGTGAAAACTCAGAA 600
Db 545 GATGCAAAATATGTTGTAAGAGAAAGCAATTTTAAAGTCTTTTCTGTGAAAACTCAGAA 604
QY 601 TCGAGTCTGTGGAGACCTCGAGACAGACATGTTGGATGTGTGACACCTTTCTAT 660
Db 605 TCGAGTCTGTGGAGACCTCGAGACAGACATGTTGGATGTGTGACACCTTTCTAT 664
QY 661 ACAGCTTACAGACAGACAGATGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 720
Db 665 ACAGCTTACAGACAGACAGATGGGAAATTCATGCTGTGTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGACCTCTGATCAAAAGACCTTGACATTAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
Db 725 TACGACCTCTGATCAAAAGACCTTGACATTAAGTCTGATGAACCTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTGTGCAAAAGACGAAAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTGTGCAAAAGACGAAAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGACGACAGATGCTGTGTGACGCTGCTTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGACAGATGCTGTGTGACGCTGCTTCTGACTTTT 904
QY 901 GAGAGATTTGTCATCATGATCACAACAAGAAAGGAGGCTGCTTTATGACAGAGAGAG 960
Db 905 GAGAGATTTGTCATCATGATCACAACAAGAAAGGAGGCTGCTTTATGACAGAGAGAG 964
QY 961 CAGAGCTGAGGCGCCCGCTGACCTGCTGTAAACACCCAGCCATCCCTTTCTTC 1020
Db 965 CAGAGCTGAGGCGCCCGCTGACCTGCTGTGTAAACACCCAGCCATCCCTTTCTTC 1024
QY 1021 AAAAGGATCTTTTATAGAGAAACACACAGTGAAGATCTTGAAGAAATTTGATTCAGC 1080
Db 1025 AAAAGGATCTTTTATAGAGAAACACACAGTGAAGATCTTGAAGAAATTTGATTCAGC 1084
QY 1081 CGGGAAGAGATTTATCACTTAAGTCAATTAATCAATTTGAAGATTTGAAGT 1140
Db 1085 CGGGAAGAGATTTATCACTTAAGTCAATTAATCAATTTGAAGATTTGAAGT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

```

```

RESULT 7
AAS63555
ID AAS63555 standard: cDNA: 1621 BP.
AC AAS63555:
XX
XX 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA sequence #107.
DE
XX

```

```

KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
OS
XX
XX MO200173032-A2.
FN
XX
XX 04-OCT-2001.
PE
XX
XX 27-MAR-2001; 2001WO-US09919.
PR
XX
XX 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kelos MD;
PI Fanger GR, Keltner MW, Stolk JA, Day CH, Vedvik TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
XX WPI: 2001-639232/73.
XX
XX P-PSDB: AAU69761.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 264-265; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
XX polynucleotides, polypeptides, fusion proteins of the polypeptides,
XX antibodies raised against the polypeptides (or antigenic epitopes
XX derived from them) and antigen-presenting cells expressing the
XX polypeptides. The antibodies are useful for detecting the presence of
XX cancer, especially prostate cancer. The polypeptides, polynucleotides and
XX the antigen-presenting cells are useful for stimulating and/or expanding
XX T cells specific for a tumour protein, and for inhibiting the development
XX of cancer especially prostate cancer. Compositions comprising the
XX polynucleotide and/or polypeptide are useful for stimulating an immune
XX response, and for treating cancer. The oligonucleotide is useful for
XX detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.
XX
XX
XX Sequence 1621 BP: 461 A; 330 C; 412 G; 418 T; 0 other:
XX
XX
XX Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1 ATGCACTCAGAGGATCTCGGTGTGAGCTGTCGGGCTGGCCGCGGCTTGT 60
XX
XX 5 ATGGCACTCAGAGGATCTCGGTGTGAGCTGTCGGGCTGGCCGCGGCTTGT 64
XX
XX 61 GGTATGCTCTGCTGATTTGGGGGCGCGGTGTGACGCGTGAACCGGCGGCTCCCG 120
XX
XX 65 GCTATGCTCTGCTGATTTGGGGGCGCGGTGTGACGCGTGAACCGGCGGCTCCCG 124
XX
XX 121 TACGAGTGAAGCGCTTGGGCGGCGGCAAGCGTGTGCTGTGAGTGAACGAGCCG 180
XX
XX 125 TACGAGTGAAGCGCTTGGGCGGCGGCAAGCGTGTGCTGTGAGTGAACGAGCCG 184
XX
XX 181 CGGGAAGCGCGGCTGTGCGGCGTGTGCAAGCGTGTGATGTGTGTGAGCCCTTC 240
XX
XX 185 CGGGAAGCGCGGCTGTGCGGCGTGTGCAAGCGTGTGATGTGTGTGAGCCCTTC 244
XX
XX 241 CGCGCGGTGTCATGAGAAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAATCCA 300
XX
XX

```

Db 245 CGCCGCGGTGTCATGAGAAATCCAGCTGGGCCACAGATTTGCAAGCGGGAAATCA 304
 QY AGCCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAACTCTGCGGTTAGCT 360
 XX |||||||
 Db 305 AGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAACTCTGCGGTTAGCT 364
 QY 361 GGCACAGATATCAACTATTTGGCTTTGTCAGAGTGTCTCTCAAAAATTTGGCAGAGTGT 420
 Db 365 GGCACAGATATCAACTATTTGGCTTTGTCAGAGTGTCTCTCAAAAATTTGGCAGAGTGT 424
 QY 421 GAGAAATCCGATATGCCGCGGAATCTCCTGGCTACTTTGGTGGTGGCTTATGCT 480
 Db 425 GAGAAATCCGATATGCCGCGGAATCTCCTGGCTACTTTGGTGGTGGCTTATGCT 484
 QY 481 GCACTGGCATTTAATATGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAAGTCAAT 540
 Db 485 GCACTGGCATTTAATATGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAAGTCAAT 544
 QY 541 GATGCAAAATATGTTGGAAGACAGCATATTTAAAGTTCTTTTCTGTGGAATACTCAGAAA 600
 Db 545 GATGCAAAATATGTTGGAAGACAGCATATTTAAAGTTCTTTTCTGTGGAATACTCAGAAA 604
 QY 601 TCGAGTGTGGGAAGACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTTCTAT 660
 Db 605 TCGAGTGTGGGAAGACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTTCTAT 664
 QY 661 ACGACTTACAGAGACAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720
 Db 665 ACGACTTACAGAGACAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 724
 QY 721 TAGCAGTGTGATCAAAAGCACTTGGACTTAAGTCTGATGACTTCCCAATCAGATAGC 780
 Db 725 TAGCAGTGTGATCAAAAGCACTTGGACTTAAGTCTGATGACTTCCCAATCAGATAGC 784
 QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAATTTGCAGATGATTTGCAAGAAGACGAG 840
 Db 785 ATGATGATTTGGCCAGAAATGAAGAAGAATTTGCAGATGATTTGCAAGAAGACGAG 844
 QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCAGATGCTGTGTGACTCGGTTCTGACTTTT 900
 Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCAGATGCTGTGTGACTCGGTTCTGACTTTT 904
 QY 901 GAGAGAGTGTGTCAATGATCACAACAAGAGAGCGGCTGTTTATCACCAGTGAAGAG 960
 Db 905 GAGAGAGTGTGTCAATGATCACAACAAGAGAGCGGCTGTTTATCACCAGTGAAGAG 964
 QY 961 CAGAGAGTGAAGCCCGCCCTGACACTGTGCTTTAAACCCCGAGCATGCCCTTTTTC 1020
 Db 965 CAGAGAGTGAAGCCCGCCCTGACACTGTGCTTTAAACCCCGAGCATGCCCTTTTTC 1024
 QY 1021 AAAAGGATCCTTTCATAGAGAAACACACTGAGAGATACTTGAAGAATTTGATTCAGC 1080
 Db 1025 AAAAGGATCCTTTCATAGAGAAACACACTGAGAGATACTTGAAGAATTTGATTCAGC 1084
 QY 1081 CGCGAAGAGATTTATCAGCTTAAGTCAATGTAAGTAAAGTAAAGT 1140
 Db 1085 CGCGAAGAGATTTATCAGCTTAAGTCAATGTAAGTAAAGTAAAGT 1144
 QY 1141 AGTCTC 1146
 Db 1145 AGTCTC 1150

RESULT 8
 AAS10106
 ID AAS10106 standard; cDNA; 1621 BP.
 XX AAS10106;
 AC AAS10106;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human prostate tumour cDNA FI-12 #3.
 XX

KW Human; prostate tumour protein; prostate cancer; ss.
 OS Homo sapiens.
 XX
 PN US626245-B1.
 XX
 PD 17-JUL-2001.
 PF 25-FEB-1998; 98US-0030607.
 XX
 PR 25-FEB-1997; 97US-080609.
 PR 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC;
 DR WPI; 2001-440862/47.
 DR P-PSDB; AA004959.
 XX
 PT Novel polynucleotide encoding polypeptide comprising a portion of
 PT prostate tumour protein useful for inhibiting development of prostate
 CC cancer or for treating prostate cancer in a patient.
 XX
 PS Claim 1; Column 112-113; 105pp; English.
 XX
 CC The sequence is a human prostate tumour cDNA which encodes a
 CC partial tumour protein. The DNA is useful for inhibiting the development
 CC of prostate cancer or for treating prostate cancer in a patient.
 XX
 SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
 XX

Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
 Best local similarity 99.8%; Pred. No. 0;
 Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAAGGCGATCTCGTGTGAGAGCTGCGGCTGGCCCGGCGCTGTCT 60
 Db 5 ATGGCACTGCAAGGCGATCTCGTGTGAGAGCTGCGGCTGGCCCGGCGCTGTCT 64
 QY 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 65 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
 QY 121 TAGCAGTGAAGCCGCTTGGGCGGCGCAAGCGCTGCTAGTGTGAGCTGAAGCAGCG 180
 Db 125 TAGCAGTGAAGCCGCTTGGGCGGCGCAAGCGCTGCTAGTGTGAGCTGAAGCAGCG 184
 QY 181 CGGGAGCCGCGCTGCTGCGGCGCTGTGTGCAAGCGGTGAGTGTGTGAGAGCCCTTC 240
 Db 185 CGGGAGCCGCGCGCTGCTGCGGCGCTGTGTGCAAGCGGTGAGTGTGTGAGAGCCCTTC 244
 QY 241 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 245 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
 QY 301 AGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAACTCTCCGTTAGCT 360
 Db 305 AGGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAACTCTCCGTTAGCT 364
 QY 361 GGCACAGATATCAACTATTTGGCTTTGTCAGAGTGTCTCTCAAAAATTTGGCAGAGTGT 420
 Db 365 GGCACAGATATCAACTATTTGGCTTTGTCAGAGTGTCTCTCAAAAATTTGGCAGAGTGT 424
 QY 421 GAGAAATCCGATATGCCGCGGAATCTCCTGGCTACTTTGGTGGTGGCTTATGCT 480
 Db 425 GAGAAATCCGATATGCCGCGGAATCTCCTGGCTACTTTGGTGGTGGCTTATGCT 484
 QY 481 GCACTGGCATTTAATATGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAAGTCAAT 540
 Db 485 GCACTGGCATTTAATATGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAAGTCAAT 544

OY	541	GATGCAAAATATGCTGGAGGACACGATATTTATATCTCTTTCTGTGGAAATCTCAGAA	600
Db	545	GATGCAAAATATGCTGGAGGACACGATATTTATATCTCTTTCTGTGGAAATCTCAGAA	604
OY	601	TTCAGCTCTGTGGAAACACCTCCGAGGACGAACATGTTGATGATGGTGGAGACCTTTCTAT	660
Db	605	TTCAGCTCTGTGGAAACACCTCCGAGGACGAACATGTTGATGATGGTGGAGACCTTTCTAT	664
OY	661	ACGACTTACAGACACGACGATGGGGATTCATGCTGTTGGAGCAATAGAACCCAGTTTC	720
Db	665	ACGACTTACAGACACGACGATGGGGATTCATGCTGTTGGAGCAATAGAACCCAGTTTC	724
OY	721	TACGACCTCTGATCAAAAGCATTTGACATTAAGTCTGATGAACCTTCCCAATCAGATGAC	780
Db	725	TACGACCTCTGATCAAAAGCATTTGACATTAAGTCTGATGAACCTTCCCAATCAGATGAC	784
OY	781	ATGAGATGATTTGGCCGAAATAGAAAGAAAGTTTGGCAGATGATTTTGGCAAGAGCAGAG	840
Db	785	ATGAGATGATTTGGCCGAAATAGAAAGAAAGTTTGGCAGATGATTTTGGCAAGAGCAGAG	844
OY	841	GCAGAGTGTGTCAAAATCTTTGAGCGGCACAGATGCGCTGTGACTCCGTTCTGACTTTT	900
Db	845	GCAGAGTGTGTCAAAATCTTTGAGCGGCACAGATGCGCTGTGACTCCGTTCTGACTTTT	904
OY	901	GAGAGAGTTGTTCATCATGATCATCAACAAGAGAACGGGCTGTTATCACCACTGAGAG	960
Db	905	GAGAGAGTTGTTCATCATGATCATCAACAAGAGAACGGGCTGTTATCACCACTGAGAG	964
OY	961	CAGAGCTAGAGCCCCCGCCGCGACCTGTGCTGTTTAAACACCCGACATCCCTTTTTC	1020
Db	965	CAGAGCTAGAGCCCCCGCCGCGACCTGTGCTGTTTAAACACCCGACATCCCTTTTTC	1024
OY	1021	AAAAGGATCTCTTATAGAGAAACACACTGAGAGAGATCTGAAGAAATTTGGATTCAAC	1080
Db	1025	AAAAGGATCTCTTATAGAGAAACACACTGAGAGAGATCTGAAGAAATTTGGATTCAAC	1084
OY	1081	CGGGAAGATATTTATACACTTAATCTCAGATTAATATCATTTGAAGTAATAGTAAAGCT	1140
Db	1085	CGGGAAGATATTTATACACTTAATCTCAGATTAATATCATTTGAAGTAATAGTAAAGCT	1144
OY	1141	AGTCTC 1146	
Db	1145	AGTCTC 1150	
RESULT 9			
AAH93463			
ID	AAH93463 standard: CDNA: 1621 BP.		
XX	AAH93463;		
AC			
XX			
DT	04-OCT-2001 (first entry)		
XX			
XX	Human prostate-specific full length cDNA sequence FI-12.		
DE			
XX			
KW	Human: prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cytostatic; gene therapy; metastasis; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200151633-A2.		
XX			
PD	19-JUL-2001.		
XX			
PF	16-JAN-2001; 2001WO-US01574.		
XX			
PR	14-JAN-2000; 2000US-0483672.		
XX			
RA	(CORI-) CORIAX CORP.		
XX			
FI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;		
PI	Kaios MD, Fanger GR, Day CH, Retter WM, Stolk JA, Skeiky YAW;		
	Wang A, Meagher MJ;		

XX	WP1; 2001-425673/45.
DR	
XX	New polynucleotide encoding a prostate-specific protein, for
PT	diagnosing, monitoring and treating prostate cancer in a patient and
PT	for use in vaccines -
XX	
XX	Claim 1; Page 262-263; 543pp: English.
P5	
XX	The present invention describes polynucleotide sequences (I) which encode
CC	prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC	and can be used in vaccine production and gene therapy. (I), (II),
CC	antibodies to (II), fusion proteins comprising (II), and isolated
CC	T cells prepared using (I) or (II) are used treat cancer in a patient.
CC	(I) and the antibodies are also used in the detection of cancer in a
CC	patient. The cancer that is diagnosed or treated is particularly
CC	prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC	(I) can be used for monitoring the progression of cancer in a patient.
CC	(I) and (II) can also be used to improve diagnostic and therapeutic
CC	methods for prostate cancer. They can indicate the level of metastasis
CC	as well as the prostate volume. AH93357 to AAH93944 and AAM01115 to
CC	AAM01318 represent polynucleotide and amino acid sequences used in the
CC	exemplification of the present invention.
xx	
SQ	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
	Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
	Best Local Similarity 99.8%; Pred. No. 0;
	Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	
OY	1 ATGGCACTCAGGACATCGTGGTCGTGAAGCTGCCGCCGCCGCCGCCGTTCTGT 60
OY	5 ATGGCACTCAGGACATCGTGGTCGTGAAGCTGCCGCCGCCGCCGCCGTTCTGT 64
OY	
OY	61 GCATAGCTGCCTGCGACTTCGGGGCGCTGTGTGACGCTGACGCCGCCGCCGCC 120
OY	65 GCATAGCTGCCTGCGACTTCGGGGCGCTGTGTGACGCTGACGCCGCCGCCGCC 124
OY	
OY	121 TAGCACGTAGCCGCTTGCGCCGGGGCAAGCCTTGCTA GTCTGGAAGCAAGCCG 180
OY	125 TAGCACGTAGCCGCTTGCGCCGGGGCAAGCCTTGCTA GTCTGGAAGCAAGCCG 184
OY	
OY	181 CGGGAGCCGCGCTGTGCGGCTGTGTGCAAGCGGTGGATGCTGTGAGACCCTTC 240
OY	185 CGGGAGCCGCGCTGTGCGGCTGTGTGCAAGCGGTGGATGCTGTGAGACCCTTC 244
OY	
OY	241 CGCGCGGCTGTATGGAGAACAATCCACGCTGGGGCCCGAAGATTCTGCAGCGGGAATAATCA 300
OY	245 CGCGCGGCTGTATGGAGAACAATCCACGCTGGGGCCCGAAGATTCTGCAGCGGGAATAATCA 304
OY	
OY	301 AGCCTTAATTTATGCCAGGCTGATGATTTGGGCCAGTACAGAAAGCTTCTGCCGTTTACT 360
OY	305 AGCCTTAATTTATGCCAGGCTGATGATTTGGGCCAGTACAGAAAGCTTCTGCCGTTTACT 364
OY	
OY	361 GGCCACGATATCACTATTGGCTTTGGTGTAGTGTTCCTCAAAAATTTGGCAAGTAGGT 420
OY	365 GGCCACGATATCACTATTGGCTTTGGTGTAGTGTTCCTCAAAAATTTGGCAAGTAGGT 424
OY	
OY	421 GAATAATCGGTATGCCCGGTGATATCTCGGTGATCTGCTGTGTTGGTGGGCTTATGTGT 480
OY	425 GAATAATCGGTATGCCCGGTGATATCTCGGTGATCTGCTGTGTTGGTGGGCTTATGTGT 484
OY	
OY	481 GCACTGGGATATATATGCTCTTTTGAACCGCACAGCACTGGCAAGGTTAGGTACTT 540
OY	485 GCACTGGGATATATATGCTCTTTTGAACCGCACAGCACTGGCAAGGTTAGGTACTT 544
OY	
OY	541 GATGCAATATGTGTGAAGAACAGCATATTTAAGTTCTTTCTGTGAAAACTACAGAA 600
OY	545 GATGCAATATGTGTGAAGAACAGCATATTTAAGTTCTTTCTGTGAAAACTACAGAA 604
OY	
OY	601 TCAGAGCTGTGTGGGAAGACCTCGAGACAGAAACATGTTGGATGGTGTGAGCACCTTTCTAT 660
OY	605 TCAGAGCTGTGTGGGAAGACCTCGAGACAGAAACATGTTGGATGGTGTGAGCACCTTTCTAT 664

OY	661	ACGACTTACAGACACGACGATGGGGAATTCATTCGCTGTGGAGCAATATGAACCCAGTTC	72
OY	665	ACGACTTACAGACACGACGATGGGGAATTCATTCGCTGTGGAGCAATATGAACCCAGTTC	72
OY	721	TACGAGCTGCTGATCAAGAGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC	78
Db	725	TACGAGCTGCTGATCAAGAGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC	78
OY	781	ATGGATGATTTGGCCAGAAATGAGAAGAATTTCAGATGATATTTGCAAAGAAGACGAG	84
Db	785	ATGGATGATTTGGCCAGAAATGAGAAGAATTTCAGATGATATTTGCAAAGAAGACGAG	84
OY	841	GCAGAGCTGTGTCGAATTTTGGACGGGCACACATGCTCTGTGACATCCGGTTCTGACTTT	90
Db	845	GCAGAGCTGTGTCGAATTTTGGACGGGCACACATGCTCTGTGACATCCGGTTCTGACTTT	90
OY	901	GAGGAGGTTGTTTCATCATGATCATCAACAAGGAACGGGCTCGTTATATCAGCAGTGAGAG	96
Db	905	GAGGAGGTTGTTTCATCATGATCATCAACAAGGAACGGGCTCGTTATATCAGCAGTGAGAG	96
OY	961	CAGACGTGAGCCCCCGCCCTGACACTCTGCTGTTTAAACACCCAGCCATCCCTCTTTC	102
Db	965	CAGACGTGAGCCCCCGCCCTGACACTCTGCTGTTTAAACACCCAGCCATCCCTCTTTC	102
OY	1021	AAAAGGATCCCTTCATATGAGGAACACACTGAGAGATATCTGGAAGATTTTGATTCAGC	108
Db	1025	AAAAGGATCCCTTCATATGAGGAACACACTGAGAGATATCTGGAAGATTTTGATTCAGC	108
OY	1081	CGCGAAGAGATTATACACTTAACCTCAAGTAAATCATTTGAAAGTAATAGGTAAAGCT	114
Db	1085	CGCGAAGAGATTATACACTTAACCTCAAGTAAATCATTTGAAAGTAATAGGTAAAGCT	114
OY	1141	AGTCTC 1146	
Db	1145	AGTCTC 1150	
RESULT 10			
AAH84777			
ID	AAH84777	standard; cDNA; 1621 BP.	
XX	AAH84777;		
AC			
XX			
DF	25-SEP-2001	(first entry)	
XX			
DE		Human prostate-specific cDNA sequence F1-12/P504S.	
XX			
KW		Human; prostate cancer; therapy; diagnosis; cat eye syndrome;	
KW		chromosome 22q11.2; prostate-specific protein; chromosome 1;	
KW		prostate specific antigen; PSA; ss.	
OS		Homo sapiens.	
XX			
PN	WO200134802-A2.		
PD	17-MAY-2001.		
XX			
PF	09-NOV-2000; 2000WO-US30904.		
XX			
PR	12-NOV-1999; 99US-0439313.		
PR	18-NOV-1999; 99US-0443686.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Xu J, Dillon DC, Mitcham JU, Harlocker SL, Jiang Y, Reed SG;		
XX	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;		
DR	WPI: 2001-308785/32.		
PT	Isolated polypeptide comprising at least an immunogenic portion of a		
PT	prostate-specific protein, useful in the diagnosis and therapy of		
PT	prostate cancer -		

XX	Claim 5; Page 162-163; 325pp; English.
XX	The present invention describes an isolated polypeptide (P1) comprising
CC	at least an immunogenic portion of a prostate-specific protein, or its
CC	variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC	(N1) have cytostatic activity and can be used in vaccine production.
CC	The polypeptides, nucleic acids and antibodies from the present
CC	invention are useful in the diagnosis and therapy of prostate cancer.
CC	Prostate specific genes P704p, P712p, P774p, P775p and B305d are located
CC	in a genomic region on chromosome 24q11.2 known as the Cat Eye Syndrome
CC	region. Prostate specific antigen (PSA) P5015 was located on
CC	chromosome 1. AAH48471 to AAH51513 and AAG59000 to AAG59077 represent
CC	polynucleotide and polypeptide sequences used in the exemplification
CC	of the present invention.
XX	
XX	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
XX	
XX	Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
XX	Best Local Similarity 99.8%; Pred. No. 0;
XX	Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 ATGGCACTGCAGAGGCATCTCGSTCTGGAAGCTGTCCGGCCTTGGCCCCCGGCTTCTGT 60
DB	5 ATGGCACTGCAGAGGCATCTCGGTCTCATGAGAGCTGTCCGGCCTTGGCCCCCGGCTTCTGT 64
QY	61 GGTATGGTCCCTGGCGAGCTTGGGGGGGGGTGTGTAGCGTGGAGACCGGCGCGGCTCCGC 120
DB	65 GCTATGGTCTTGGCTGACTTCCGGGGCGGCTGTGGTACCGCTGTGACCGGCGCGGCTCCGC 124
QY	121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCGC 180
DB	125 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCGC 184
QY	181 CGGGAGGCGCGCGTCTCGCGCTGTGTGTGCAAGGGGTGGATGTCTGTGAGCGCTTC 240
DB	185 CGGGAGGCGCGCGTCTCGCGCTGTGTGTGCAAGCGGTGTGTGTGTGTGTGTGTGTGT 244
QY	241 CGCCCGGCTGTCTATGAGAAACTCCAGCTGTGGGCCCGAGAGATTCTGCACGGGAAATCCA 300
DB	245 CGCCCGGCTGTCTATGAGAAACTCCAGCTGTGGGCCCGAGAGATTCTGCACGGGAAATCCA 304
QY	301 AGGCTATTATTATGACGAGCTGATGTGATTTGGCCAGTACAGAAAGCTTGTCCGGTTACT 360
DB	305 AGGCTATTATTATGACGAGCTGATGTGATTTGGCCAGTACAGAAAGCTTGTCCGGTTACT 364
QY	361 GGCACAGATATCACTATTGGCTTGTGAGTGTCTCTCTCAAAATTTGGAGAAAGTGT 420
DB	365 GGCACAGATATCACTATTGGCTTGTGAGTGTCTCTCTCAAAATTTGGAGAAAGTGT 424
QY	421 GAGAAATCCGATATGCCCCGTGATCTCCTGGCTGACTTTGCTGGTGGCTTATATGTGT 480
DB	425 GAGAAATCCGATATGCCCCGTGATCTCCTGGCTGACTTTGCTGGTGGCTTATATGTGT 484
QY	481 GCACGGGCGATTATATATGGCTCTTTTGGCCGACACGACACTGGCAAGGTCAGTCAAT 540
DB	485 GCACGGGCGATTATATATGGCTCTTTTGGCCGACACGACACTGGCAAGGTCAGTCAAT 544
QY	541 GATGCAAAATATGTGTGAAGAAACACCATATTTAAGTCTTTTGTGTGAAAACTCAGAAA 600
DB	545 GATGCAAAATATGTGTGAAGAAACACCATATTTAAGTCTTTTGTGTGAAAACTCAGAAA 604
QY	601 TCGAATCTGTGTGGAAGACACTTCGAGGACAGAAACATGTTGATGTGTGAGACACTTTTAT 660
DB	605 TCGAATCTGTGTGGAAGACACTTCGAGGACAGAAACATGTTGATGTGTGAGACACTTTTAT 664
QY	661 ACGACTTACAGAGACAGCATGGGAAATTCATAGCTGTGTGAGCAATAGAACCCGACTTC 720
DB	665 ACGACTTACAGAGACAGCATGGGAAATTCATAGCTGTGTGAGCAATAGAACCCGACTTC 724
QY	721 TACGAGCTGTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCAAATCAGATGAC 780
DB	725 TACGAGCTGTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCAAATCAGATGAC 784

QY 781 ATGATGATTTGGCCAGAAATGAGAAAGATTGTCAGATGATTTTGCAGAAAGAGAG 840
DB 785 ATGATGATTTGGCCAGAAATGAGAAAGATTGTCAGATGATTTTGCAGAAAGAGAG 844
QY 841 GCAGAGTGGTGAATCTTTTACGCGACAGATGCTGTGTGCTCCGGTTCGACTTTT 900
DB 845 GCAGAGTGGTGAATCTTTTACGCGACAGATGCTGTGTGCTCCGGTTCGACTTTT 904
QY 901 GAGAGTGTTCATCATGATGATGACAGAAAGAGGGGCTGTTTATCAGATGAGAG 960
DB 905 GAGAGTGTTCATCATGATGATGACAGAAAGAGGGGCTGTTTATCAGATGAGAG 964
QY 961 CAGAGCTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCATCCCTTCTTTC 1020
DB 965 CAGAGCTGAGCCCGCCCTGACCTCTGCTGTTAAACACCCAGCATCCCTTCTTTC 1024
QY 1021 AAAAGGATCTTTTCTATGAGACACACAGATGAGATGATTTGATTTGAGC 1080
DB 1025 AAAAGGATCTTTTCTATGAGACACACAGATGAGATGATTTGATTTGAGC 1084
QY 1081 CGCGAAGATTTATCAGCTTAACCTCAGATTAATCATTTGAAGTAAGTAAGCT 1140
DB 1085 CGCGAAGATTTATCAGCTTAACCTCAGATTAATCATTTGAAGTAAGTAAGCT 1144
QY 1141 AGTCTC 1146
DB 1145 AGTCTC 1150

RESULT 11
AAH02528
ID AAH02528 standard; cDNA; 1621 BP.
AC AAH02528;
XX
XX 14-JUN-2001 (first entry)
DE Prostate tumour antigen determined full length cDNA sequence for Fl-12.
XX
XX Human: prostate tumour antigen; prostate tumour; therapy: diagnosis;
XX prostate cancer; immunogenic; cytostatic; vaccine; ss.
OS Homo sapiens.
XX
XX MO200125272-A2.
PD 12-APR-2001.
XX
XX 04-OCT-2000; 2000MO-US27464.
PF
XX 04-OCT-1999; 990S-0157455.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Skelky YAW, Reed SC, Cheever MA;
PI WPI: 2001-245062/25.
DR P-PSDB; AAB4798.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer.
XX
XX Claim 4; Page 153; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a

CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB4798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCACTGACAGGCGATCTCGCTGAGCTGTCGGCCCTGCGCCCGCTTCTGT 60
DB 5 ATGGCACTGACAGGCGATCTCGCTGAGCTGTCGGCCCTGCGCCCGCTTCTGT 64
QY 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 65 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
QY 121 TACGACGTGAGCCGCTTGGGCGCGGCGCAAGCGCTGCTAGTGTGAGACTGAGCAGCCG 180
DB 125 TACGACGTGAGCCGCTTGGGCGCGGCGCAAGCGCTGCTAGTGTGAGACTGAGCAGCCG 184
QY 181 CGGGAGCCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 185 CGGGAGCCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 241 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 245 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
QY 301 AGCTTATTTATGCGAGCGTGAATGATTTGGCGTACAGAACTTCTGCGGTATAGCT 360
DB 305 AGCTTATTTATGCGAGCGTGAATGATTTGGCGTACAGAACTTCTGCGGTATAGCT 364
QY 361 GCGCAGATATCAACTATTTGGCTTTGCTGAGCTGCTTCTCTCAAAAATTTGCAAGTGGT 420
DB 365 GCGCAGATATCAACTATTTGGCTTTGCTGAGCTGCTTCTCTCAAAAATTTGCAAGTGGT 424
QY 421 GAGAACTCGATAGCCCGCGTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 425 GAGAACTCGATAGCCCGCGTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
QY 481 GCAGTGGGCAATTAATGAGCTTTTGAACCGCACACGCTGCAAGGGTCAAGTCAAT 540
DB 485 GCAGTGGGCAATTAATGAGCTTTTGAACCGCACACGCTGCAAGGGTCAAGTCAAT 544
QY 541 GATGCAAAATATGCTGGAAGGACAGCATTTTAAGTCTTTTCTGCGAAACCTCAGAAA 600
DB 545 GATGCAAAATATGCTGGAAGGACAGCATTTTAAGTCTTTTCTGCGAAACCTCAGAAA 604
QY 601 TCGAGCTGCGGGAAGCACTCGAGGACAGAACTGTTGATGTTGAGGACCTTCTAT 660
DB 605 TCGAGCTGCGGGAAGCACTCGAGGACAGAACTGTTGATGTTGAGGACCTTCTAT 664
QY 661 ACGACTTACAGACAGCAGATGGGGAATTCATGCTGTTGAGCAATAGAACCCAGTTC 720
DB 665 ACGACTTACAGACAGCAGATGGGGAATTCATGCTGTTGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCAATGAGTAC 780
DB 725 TACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCAATGAGTAC 784
QY 781 ATGATGATTTGGCCAGAAATGAGAAAGATTGTCAGATGATTTTGCAGAAAGAGAG 840
DB 785 ATGATGATTTGGCCAGAAATGAGAAAGATTGTCAGATGATTTTGCAGAAAGAGAG 844
QY 841 GCAGAGTGGTGAATCTTTTACGCGACAGATGCTGTGTGCTCCGGTTCGACTTTT 900
DB 845 GCAGAGTGGTGAATCTTTTACGCGACAGATGCTGTGTGCTCCGGTTCGACTTTT 904
QY 901 GAGAGGTTTTCATCATGATGATGACAGAAAGAGGGGCTGTTTATCAGACTGAGAG 960


```

Db 605 TCGAGCTGTGGGAGACACCTCGAGAGACAGACATGTTGGATGTGACACCTTTCTAT 664
Oy 661 ACGACTTACAGAGACACAGATGGGGAATTCATGGCTTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGAGACACAGATGGGGAATTCATGGCTTTGGAGCAATAGAACCCAGTTC 724
Oy 721 TACGAGCTGTGATCAAAAGACTTGACTAAAGCTGATGATACCTTCCCAATGATGAGC 780
Db 725 TACGAGCTGTGATCAAAAGACTTGACTAAAGCTGATGATACCTTCCCAATGATGAGC 784
Oy 781 ATGATGATGGCCAGCAATGAAGAAGATTGGACATGATTTTCCAAAGACGAG 840
Db 785 ATGATGATGGCCAGCAATGAAGAAGATTGGACATGATTTTCCAAAGACGAG 844
Oy 841 GCAAGTGTGTCAAAATCTTTACGGCACAATGCTGTGACTCCGTTCTGACTTT 900
Db 845 GCAAGTGTGTCAAAATCTTTACGGCACAATGCTGTGACTCCGTTCTGACTTT 904
Oy 901 GAGAGCTTTTCATCATGATCACAACAAGAGACGGGCTCGTTTATCACAGTAGAGAG 960
Db 905 GAGAGCTTTTCATCATGATCACAACAAGAGACGGGCTCGTTTATCACAGTAGAGAG 964
Oy 961 CAGAGCTGAGCCCGCCCTGACCTCTGCTTTAAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGAGCTGAGCCCGCCCTGACCTCTGCTTTAAACACCCAGCCATCCCTTCTTC 1024
Oy 1021 AAAGAGATCTTTCATAGAGACACACATGAGATCTTGAAGATTTGGATTACG 1080
Db 1025 AAAGAGATCTTTCATAGAGACACACATGAGATCTTGAAGATTTGGATTACG 1084
Oy 1081 CGGCAAGATTTTATGAGCTTAACTCAATCAATTAAGTAAAGTAAAGTAAAGT 1140
Db 1085 CGGCAAGATTTTATGAGCTTAACTCAATCAATTAAGTAAAGTAAAGTAAAGT 1144
Oy 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 13
ABV21293
ID ABV21293 standard; cDNA: 2376 BP.
XX
AC ABV21293;
XX
DE 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21284.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PM WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001, 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183119P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.

```

```

XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 3532; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement; (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SO Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other:

Query Match          99.7%; Score 1142.8; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ATGGCACTGAGGCAATCGGTGCTGAGCTGCGGCTGGCCCGGCGGCTTCGT 60
Db 101 ATGGCACTGAGGCAATCGGTGCTGAGCTGCGGCTGGCCCGGCGGCTTCGT 160
Oy 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 161 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 220
Oy 121 TACGAGCTGAGCCGCTTGGGCGGCGCAAGCGCTCGCTAGCTGAGACCTGAAGCAGCG 180
Db 221 TACGAGCTGAGCCGCTTGGGCGGCGCAAGCGCTCGCTAGCTGAGACCTGAAGCAGCG 280
Oy 181 CGGGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 281 CGGGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340
Oy 241 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 341 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
Oy 301 AGGCTTATTTATGCGCAGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTACT 360
Db 401 AGGCTTATTTATGCGCAGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTACT 460
Oy 361 GCGCAGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGCGAAGATGCT 420
Db 461 GCGCAGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGCGAAGATGCT 520
Oy 421 GAGAATCCGATGCCCCCGGTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 521 GAGAATCCGATGCCCCCGGTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 580
Oy 481 GCACTGGCATTAATAATGAGCTTTTGGACGCAACAGCACTGGCAAGGCTCAGTCAATT 540
Db 581 GCACTGGCATTAATAATGAGCTTTTGGACGCAACAGCACTGGCAAGGCTCAGTCAATT 640
Oy 541 GATGCAAAATATGTTGGTGAAGAAAGCAATATTTAAGTCTTTCTGTGGAAAAATCACA 600
Db 641 GATGCAAAATATGTTGGTGAAGAAAGCAATATTTAAGTCTTTCTGTGGAAAAATCACA 700
Oy 601 TCGAGCTGTGGGAGACACCTCGAGGACAGACATGTTGGATGTGAGACACCTTTCTAT 660
Db 701 TCGAGCTGTGGGAGACACCTCGAGGACAGACATGTTGGATGTGAGACACCTTTCTAT 760

```

QY 661 ACGACTTACAGACAGCAGATGGGAATTCATGCTGTGTGGACAAATGAAACCCCAAGTTC 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 761 ACGACTTACAGACAGCAGATGGGAATTCATGCTGTGTGGACAAATGAAACCCCAAGTTC 820
 QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATAGATGAGC 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 821 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATAGATGAGC 880
 QY 781 ATGATGATTTGGCCAGAAATGAAAGAAAGTTTGCAGATGATTTTGCAGAAAGAGCAGAG 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 881 ATGATGATTTGGCCAGAAATGAAAGAAAGTTTGCAGATGATTTTGCAGAAAGAGCAGAG 940
 QY 841 GCAGAGTGTGTCAATCTTTGACGGCACAGATGCTGTGACCTCCGGTTTGACTTTT 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 941 GCAGAGTGTGTCAATCTTTGACGGCACAGATGCTGTGACCTCCGGTTTGACTTTT 1000
 QY 901 GAGGAGTGTGTCAATCTTTGACGGCACAGATGCTGTGACCTCCGGTTTGACTTTT 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1001 GAGGAGTGTGTCAATCTTTGACGGCACAGATGCTGTGACCTCCGGTTTGACTTTT 1060
 QY 961 CAGACGTGAGCCCCCGCCCTGACACCTCTGCTTAAACACCCCAAGCATCCCTTCTTTC 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1061 CAGACGTGAGCCCCCGCCCTGACACCTCTGCTTAAACACCCCAAGCATCCCTTCTTTC 1120
 QY 1021 AAAAGGATCTTTTATAGGAGACACACTGAGAGATCTTGAAGAATTTGGATTCAAC 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1121 AAAAGGATCTTTTATAGGAGACACACTGAGAGATCTTGAAGAATTTGGATTCAAC 1180
 QY 1081 CGCGAAGATTTTATCAGCTTAACCTCAGTAAATCATTTGAAGAATTAAGTAAAGCT 1140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1181 CGCGAAGATTTTATCAGCTTAACCTCAGTAAATCATTTGAAGAATTAAGTAAAGCT 1240
 QY 1141 AGCTTC 1146
 |||||||
 Db 1241 AGCTTC 1246
 |||||||
 RESULT 14
 ABV2181
 ID ABV2181 standard; cDNA: 2376 BP.
 AC ABV2181;
 XX
 DT 13-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 21872.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN W0200160860-A2.
 PN
 PD 23-AUG-2001.
 PD
 PF 20-FEB-2001; 2001WO-US05171.
 PF
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 PR
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 3719; 11750pp; English.
 CC
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 XX
 SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;
 Query Match 99.7%; Score 1142.8; DB 23; Length 2376;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGCGACTGCAAGGAGCATCTCGGTGAGCTGTCCGCGCCCGGCGCCGTTCTGT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 101 ATGCGACTGCAAGGAGCATCTCGGTGAGCTGTCCGCGCCCGGCGCCGTTCTGT 160
 QY 61 GCTATGCTCTGCTGACTTGGGGCGCGTGTGTACCGCTGTGACCGCCGCGCTCCGC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 161 GCTATGCTCTGCTGACTTGGGGCGCGTGTGTGTACCGCTGTGACCGCCGCGCTCCGC 220
 QY 121 TACGACGTGACCGCCTTGGGCGCGGCAAGCGCTGCTAGTGTGAGACTTAAGCAGCG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 221 TACGACGTGACCGCCTTGGGCGCGGCAAGCGCTGCTAGTGTGAGACTTAAGCAGCG 280
 QY 181 CGGGAGCCGCGCTGCTGCGCGCTGTGTGCAAGCGGCTGTGCTGTGAGCCCTTC 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 281 CGGGAGCCGCGCTGCTGCGCGCTGTGTGCAAGCGGCTGTGCTGTGAGCCCTTC 340
 QY 241 CGCGCGGTGCTATGAGAGAACTCCAGTGGGCGCCAGATTTGACAGCGGGAATCA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 341 CGCGCGGTGCTATGAGAGAACTCCAGTGGGCGCCAGATTTGACAGCGGGAATCA 400
 QY 301 AGGCTTATTTATGCGAGGCTGATGATTTGGCCAGTGTGAGAAAGCTTGTGCGGTTACT 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 401 AGGCTTATTTATGCGAGGCTGATGATTTGGCCAGTGTGAGAAAGCTTGTGCGGTTACT 460
 QY 361 GGCCAGATATCAACTATTTGGCTTGTCAAGTGTCTCTCAAAATTTGCGAAGTGT 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 461 GGCCAGATATCAACTATTTGGCTTGTCAAGTGTCTCTCAAAATTTGCGAAGTGT 520
 QY 421 GAGAAATCGTATGCGCGCTGATCTCTGCTGACTTGTGCTGTGTGTGCTTATGTGT 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 521 GAGAAATCGTATGCGCGCTGATCTCTGCTGACTTGTGCTGTGTGTGCTTATGTGT 580
 QY 481 GCACGTGGCATTTAATGATGCTTTTGTACCGCACAGCAGCTGGAGAGGTGAGTCAAT 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 581 GCACGTGGCATTTAATGATGCTTTTGTACCGCACAGCAGCTGGAGAGGTGAGTCAAT 640
 QY 541 GATGCAATATGATGAGAGAAAGCATATTTAAGTTCTTTCTGTGAAACTCAGAAA 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 641 GATGCAATATGATGAGAGAAAGCATATTTAAGTTCTTTCTGTGAAACTCAGAAA 700
 QY 601 TCGAGCTGTGGAGAGCACTCGAGAGCAGAAATGTTGATGTTGAGCACTTTCTAT 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 701 TCGAGCTGTGGAGAGCACTCGAGAGCAGAAATGTTGATGTTGAGCACTTTCTAT 760
 QY 661 ACGACTTACAGACAGCAGATGGGAATTCATGCTGTGTGGACAAATGAAACCCCAAGTTC 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 761 ACGACTTACAGACAGCAGATGGGAATTCATGCTGTGTGGACAAATGAAACCCCAAGTTC 820

QY	721	TACGACCTCTGATCAAGGACCTTGGACTAAAGTCTGATGAACTTCCCAATCAGTACG	780	CC	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
Db	821	TACGACCTCTGATCAAGGACCTTGGACTAAAGTCTGATGAACTTCCCAATCAGTACG	880	CC	specification or its complement. (I) is useful for:
QY	781	ATGAGATGATGGCCGAATAATGAATAAAGTTCGAGATCTATTGTCAAAGACGACG	840	CC	(a) assessing whether a patient is afflicted with prostate cancer;
Db	881	ATGAGATGATGGCCGAATAATGAATAAAGTTCGAGATCTATTGTCAAAGACGACG	940	CC	(b) monitoring the progression of prostate cancer in a patient;
QY	841	GCAGACTGCTGCANAATCTTTCAGCGACAGATGCTGTGATCTCGGTTCTGACTTTT	900	CC	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
Db	941	GCAGACTGCTGCANAATCTTTCAGCGACAGATGCTGTGATCTCGGTTCTGACTTTT	1000	CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
QY	901	GAGGAGCTGTTTCATCATGATCATCACACAAAGAACGGGCGCTCTTTATCATCAGCAGT	960	CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
Db	1001	GAGGAGCTGTTTCATCATGATCATCACACAAAGAACGGGCGCTCTTTATCATCAGCAGT	1060	CC	(f) assessing the prostate cell carcinogenic potential of a compound;
QY	961	CAGGAGCTGAGCCCGCCGCTGCACCTCTGTTAAACACCCGACCCATCCCTTCTTTC	1020	CC	(g) determining whether prostate cancer has metastasized in a patient;
Db	1061	CAGGAGCTGAGCCCGCCGCTGCACCTCTGTTAAACACCCGACCCATCCCTTCTTTC	1120	CC	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
QY	1021	AAAAGGATCCCTTTCATGAGAACACACATGAGAGATCTGAGGATTTGGATTGACG	1080	CC	(i) is also useful as a pharmacodynamic or pharmacogenomic marker.
Db	1121	AAAAGGATCCCTTTCATGAGAACACACATGAGAGATCTGAGGATTTGGATTGACG	1180	CC	
QY	1081	CGGGAAGATTTTATCAGCTTAATCTCAGATTAATCATTTGAAAGTATATGAGTAAAGCT	1140	QY	1
Db	1181	CGGGAAGATTTTATCAGCTTAATCTCAGATTAATCATTTGAAAGTATATGAGTAAAGCT	1240	Db	101
QY	1141	AGTCTC 1146		QY	61
Db	1241	AGTCTC 1246		Db	161
RESULT 15				QY	121
ABV25239				Db	221
ID	ABV25239	standard; cDNA; 2376 BP.		QY	181
AC	ABV25239;			Db	281
XX	16-SEP-2002	(first entry)		QY	241
DT	Human prostate expression marker	cDNA 25230.		Db	341
DE	Human prostate cancer: cytostatic; carcinogen; pharmacodynamic marker:			QY	301
XX	Human prostate cancer: cytostatic; carcinogen; pharmacodynamic marker:			Db	401
XX	pharmacogenomic marker; gene; ss.			QY	361
OS	Homo sapiens.			Db	461
XX	WO200160860-A2.			QY	421
PD	23-AUG-2001.			Db	521
XX	20-FEB-2001; 2001WO-US05171.			QY	481
PF	17-FEB-2000; 2000US-183319P.			Db	581
XX	16-MAR-2000; 2000US-189862P.			QY	541
PR	25-MAY-2000; 2000US-207454P.			Db	641
PR	09-JUN-2000; 2000US-211314P.			QY	601
PR	18-JUL-2000; 2000US-219007P.			Db	701
PR	13-DEC-2000; 2000US-255281P.			QY	761
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.			Db	821
PA	Schlegel R, Endege WO, Monahan JE.			QY	881
PI	WPI; 2001-662795/76.			Db	941
DR				QY	1001
XX	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer			Db	1061
XX	Claim 1; Page 4947-4948; 11750P; English.			QY	1121
XX				Db	1181

```

Db 821 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 880
QY 781 ATGGATGATTGGCCAGAAATGAGAGAAAGTTTGCAGATGATTTGCAAGAGAGAGAG 840
    |||||||
Db 881 ATGGATGATTGGCCAGAAATGAGAGAAAGTTTGCAGATGATTTGCAAGAGAGAGAG 940
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
    |||||||
Db 941 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 1000
QY 901 GAGGAGGTTGTCATCATGATCACAACAAGAGAGAGGGGCTGTTATCACCAGTGAGGAG 960
    |||||||
Db 1001 GAGGAGGTTGTCATCATGATCACAACAAGAGAGGGGCTGTTATCACCAGTGAGGAG 1060
QY 961 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
    |||||||
Db 1061 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1120
QY 1021 AAAAGGATCTTTCATATAGAGAACACACTGAGAGATCTTGAAGAAATTGGATTCAAC 1080
    |||||||
Db 1121 AAAAGGATCTTTCATATAGAGAACACACTGAGAGATCTTGAAGAAATTGGATTCAAC 1180
QY 1081 CGCGAAGAGATTATACAGCTTAAGTCAAGTAAATCATTTGAAGTAATAGGTAAAGCT 1140
    |||||||
Db 1181 CGCGAAGAGATTATACAGCTTAAGTCAAGTAAATCATTTGAAGTAATAGGTAAAGCT 1240
QY 1141 AGTCTC 1146
    |||||||
Db 1241 AGTCTC 1246

```

Search completed: April 1, 2003, 19:55:07
 Job time : 285.227 secs

271 TGTGCAAGCGGTGATGCTGCTGAGAGCCCTTCGCCCGGCTGATGAGAAACTCC 330
|||||
241 TGTGCAAGCGGTGATGCTGCTGAGAGCCCTTCGCCCGGCTGATGAGAAACTCC 300
|||||
331 AGCTGGCCCGAGATTCGACAGCGGAAATCCAGAGCTTATTTATGACAGCTGAGTG 390
|||||
301 AGCTGGCCCGAGATTCGACAGCGGAAATCCAGAGCTTATTTATGACAGCTGAGTG 360
|||||
391 GATTGGCCCGAGAGACTTCGCGGTTAGTGGCCAGATTCACATCATTTGGCTT 450
|||||
361 GATTGGCCCGAGAGACTTCGCGGTTAGTGGCCAGATTCACATCATTTGGCTT 420
|||||
451 TGTAGGTTCTCTCAAAAATTTGACAGATGCTGAGATCCGATGCCCGCTGATC 510
|||||
421 TGTAGGTTCTCTCAAAAATTTGACAGATGCTGAGATCCGATGCCCGCTGATC 480
|||||
511 TCTGGCTGATCTTGGCTGCTGCTTATGCTGACACTGGGCAATTAATGGCTCTTT 570
|||||
481 TCTGGCTGATCTTGGCTGCTGCTTATGCTGACACTGGGCAATTAATGGCTCTTT 540
|||||
571 TTGACCGCACACGCTGAGAGGCTCAGTTCATTTGATGCAAAATATGAGAAAGACAG 630
|||||
541 TTGACCGCACACGCTGAGAGGCTCAGTTCATTTGATGCAAAATATGAGAAAGACAG 600
|||||
631 CATATTTAACTCTTTCTGTGAAATCTCAGAAATGAGTCTGAGAAAGACAGCTGAG 690
|||||
601 CATATTTAACTCTTTCTGTGAAATCTCAGAAATGAGTCTGAGAAAGACAGCTGAG 660
|||||
691 GACGAGCATGTTGATGCTGAGAGACCTTTCTATGACACTTACAGAGACAGAGATGGG 750
|||||
661 GACGAGCATGTTGATGCTGAGAGACCTTTCTATGACACTTACAGAGACAGAGATGGG 720
|||||
751 AATTCATGCTGTTGAGCAATAGAAACCCGCTTCTACAGCTGCTGATCAAGAGACTTG 810
|||||
721 AATTCATGCTGTTGAGCAATAGAAACCCGCTTCTACAGCTGCTGATCAAGAGACTTG 780
|||||
811 GACTAAAGCTGATGAACTTCCCAATCAGATGACATGATGATGGCCAGAAATGAGA 870
|||||
781 GACTAAAGCTGATGAACTTCCCAATCAGATGACATGATGATGGCCAGAAATGAGA 840
|||||
871 AGAAGTTGCAAGTATTTGCAAAAGACGAAAGGAGAGTGTCTCAATCTTTGAGC 930
|||||
841 AGAAGTTGCAAGTATTTGCAAAAGACG--ARSGAGTGTCTCAATCTTTGAGC 899
|||||
931 GCACAGATGCTGCTGACTCCGCTTCTGACTTTTGAAGAGTGTTCATCATGATCACA 990
|||||
900 GCACAGATGCTGCTGACTCCGCTTCTGACTTTTGAAGAGTGTTCATCATGATCACA 959
|||||
991 ACAAG 995
| |
960 CAAGG 964

RESULT 3
AL575193 959 bp mRNA linear EST 16-FEB-2001
LOCUS AL575193.LT1.NFL006.PL2 Homo sapiens cDNA clone CS0D10621P05 3
DEFINITION pt1me mRNA sequence.
ACCESSION AL575193
VERSION AL575193.1 GI:12936120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source Location/Qualifiers
1. 959
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D10621P05"
/clone.lib="LT1.NFL006.PL2"
/tissue.lib="Placenta"
/note="Vector: pcMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@life.com
http://fulllength.invitrogen.com"

BASE COUNT 293 a 186 c 181 g 289 t 10 others
ORIGIN

Query Match 45.2%; Score 907; DB 9; Length 959;
Best Local Similarity 97.9%; Pred. No. 5.3e-226;
Matches 942; Conservative 6; Mismatches 10; Indels 4; Gaps 3;

1029 GACGTGAGCCCGCCGCTGACCTGCTGCTTAAACACCCGACATCCCTTCTTCAAA 1088
|||||
959 GACGTGAGCCCGC-CCTGACCTCTG--TGTAAACACCCGACATCCCTTCTTCAAA 903
|||||
1089 AGGATCTCTTCAATAGAGAAACACACAGAGATCTGGAAGATTTGGATTACAGCCG 1148
|||||
902 AGGATCTCTTCAATAGAGAAACACACAGAGATCTGGAAGATTTGGATTACAGCCG 843
|||||
1149 GAAGAGATTATACAGTTTACATGATGATTAATCATTTGAAGTAAAGTAAAGTACT 1208
|||||
842 GAAGAGATTATACAGTTTACATGATGATTAATCATTTGAAGTAAAGTAAAGTACT 783
|||||
1209 CTCTACTTCCAGGCCCGCCAGGCTCAAGTGAATTTGATATGCTATTTACAGTACAGTA 1268
|||||
782 CTCTACTTCCAGGCCCGCCAGGCTCAAGTGAATTTGATATGCTATTTACAGTACAGTA 723
|||||
1269 ACACATTAACATTTGATGATGATGAAACATGAGAGAAACATATTTACAGTCTCCACCTCT 1328
|||||
722 ACACATTAACATTTGATGATGATGAAACATGAGAGAAACATATTTACAGTCTCCACCTCT 663
|||||
1329 AATCAAGAAAGAAATTAACAGACTGATCTTCTACAGTATGATGATTAATTTAAATGATT 1388
|||||
662 AATCAAGAAAGAAATTAACAGACTGATCTTCTACAGTATGATGATTAATTTAAATGATT 603
|||||
1389 ATCATTTAGGGCTTTTGTATTAATAAATTGGGCTTCTTACTTAATTTATGATGATT 1448
|||||
602 ATCATTTAGGGCTTTTGTATTAATAAATTGGGCTTCTTACTTAATTTATGATGATT 543
|||||
1449 CTGGCTTCCAGTTTGGCTGATATATTTGTTGATATTAAGATTTCTGACTTAATTTTGA 1508
|||||
542 CTGGCTTCCAGTTTGGCTGATATATTTGTTGATATTAAGATTTCTGACTTAATTTTGA 483
|||||
1509 TGGGTTCTAGTGAAGAAAGATGATATTTCTTGAAGCATGATATACATTTATTTTACA 1568
|||||
482 TGGGTTCTAGTGAAGAAAGATGATATTTCTTGAAGCATGATATACATTTATTTTACA 423
|||||
1569 CTCTTATTTTACATGATGAAGAAATGAGAAATGCCACAAATTTGATGATTAAGATG 1628
|||||
422 CTCTTATTTTACATGATGAAGAAATGAGAAATGCCACAAATTTGATGATTAAGATG 363
|||||
1629 ACGTGAAGACAGAGTATGTTGATCCACAGGCTTTTCTTGGTGTTCATGATTCCTCT 1688
|||||
362 ACGTGAAGACAGAGTATGTTGATCCACAGGCTTTTCTTGGTGTTCATGATTCCTCT 303
|||||
1689 CTAAGCAGATTTCCAACTTTAGCAGCAGTATACACTTTTATTTTGAAGAAAGTT 1748
|||||
302 CTAAGCAGATTTCCAACTTTAGCAGCAGTATACACTTTTATTTTGAAGAAAGTT 243
|||||
1749 TCACCTGATTAATGAAATGCAATGCTTCAAGCTGAAGAAACATATTCAAATATGAGAA 1808
|||||

[illegible]

RESULT 4	
AL558977	
LOCUS	888 bp mRNA
DEFINITION	AL558977 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0d0008YK07 5
ACCESSION	AL558977
VERSION	AL558977.1 GI:12904022
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 888)
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES	Location/Qualifiers
source	1. 888

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ008YK07"
/clone_id="Tf1_NFL008_TC2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site_1: NOTI; 1st strand CDNA was primed with a NOTI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

```

Query Match	42.5%	Score 852.2	DB 9	Length 888
Best Local Similarity	99.2%	Pred. No. 1.1e-211		
Matches	862	Conservative	4	Mismatches 2
			Indels	1
			Gaps	1
QY	1	TTGAGCGCTGCTGGGCGCTAGGGCGCTGCAGTTTCTTCACGGGGCACTGGGAA	60	
Db	20	TTGAGCGCTGCTGGGCGCTAGGGCGCTGCAGTTTCTTCACGGGGCACTGGGAA	79	
QY	61	GCGCCATGGCACTGCAGGGCACTTCGTCGTGTGACACTGTCCGGCCCTGGGCCCGGGCCCGT	120	
Db	80	GCGCCATGGCACTGCAGGGCACTTCGTCGTGTGACACTGTCCGGCCCTGGGCCCGGGCCCGT	139	

OY	121	TCGTGCTATGGTCTCGACTGACTTCGGGGGCGGTGTGGTACGCTGGACGGCCGGCT	180
DB	140	TCTGTGCTATGGTCTCTGGCTGACTTCGGGGGCGCGTGTGGTACGCTGGACGGCCGGCT	199
OY	181	CCCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAAGC	240
DB	200	CCCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAAGC	259
OY	241	AGCGCGGGGAGACCGCGCGTGCCTGGGGCGCTGTGTGAACGGCGGAGATGCGTGGCTGGAGC	300
DB	260	AGCGCGGGGAGACCGCGCGTGCCTGGGGCGCTGTGTGAACGGCGGAGATGCGTGGCTGGAGC	319
OY	301	CCCTTCGGCGGCGGTGTCAATGAGAAACTCCAGACTGGGCGCCAGAGATTTCTGCAAGCGGGAAA	360
DB	320	CCCTTCGGCGGCGGTGTCAATGAGAAACTCCAGACTGGGCGCCAGAGATTTCTGCAAGCGGGAAA	379
OY	361	ATCCAGGCTTATTTTATGTCCAGGCTGAGTGGATTTGGCCAGTCCAGAGACTTCTCCGGT	420
DB	380	ATCCAGGCTTATTTTATGTCCAGGCTGAGTGGATTTGGCCAGTCCAGAGACTTCTCCGGT	439
OY	421	TAGCGGGCAGCATATCAACTATTGGGTGGTGTGACGGTGTCTCCAAATAATGGCAGAA	480
DB	440	TAGCGGGCAGCATATCAACTATTGGGTGGTGTGACGGTGTCTCCAAATAATGGCAGAA	499
OY	481	GTGTGAGAAATCCGTATGACCCCGCTGAAATCTCTCGAGTACTTTCGTGGTGGCTTTA	540
DB	500	GTGTGAGAAATCCGTATGACCCCGCTGAAATCTCTCGAGTACTTTCGTGGTGGCTTTA	559
OY	541	TGTGTGCACTGGGCAATTATATGGCTCTTTTGTGACCCGACACGACTGGCAAGGTCAAG	600
DB	560	TGTGTGCACTGGGCAATTATATGGCTCTTTTGTGACCCGACACGACTGGCAAGGTCAAG	619
OY	601	TCATGATGACCAATATGTTGGGGAAGGAACAGCAATTATTAAGTCTTTGTGTGGAAACATC	660
DB	620	TCATGATGACCAATATGTTGGGGAAGGAACAGCAATTATTAAGTCTTTGTGTGGAAACATC	679
OY	661	AGAAATCGAGTCTGTGGGAGAGCACCCTCGAGAGCAGAACATGTTGGATGGTGAGCACCTT	720
DB	680	AGAAATCGAGTCTGTGGGAGAGCACCCTCGAGAGCAGAACATGTTGGATGGTGAGCACCTT	739
OY	721	TCTATACGACTTACAGACAGCAGATGGGGAAATTCATGGCTG-TTGAAGCAATAGAACCC	779
DB	740	TCTATACGACTTACAGACAGCAGATGGGGAAATTCATGGCTGTTTGGAGCAATATARAACC	799
OY	780	CAGTCTACGAGCTCTGTATCAAAAGCACTTGGACATAAAGCTGTGATGAAGTCTCCCAATAG	839
DB	800	CAGTCTACGAGCTCTGTATCAAAAGCACTTGGACATAAAGCTGTGATGAAGTCTCCCAATAG	859
OY	840	ATGAGCATGATGATGGCCAGAAATGAA 868	
DB	860	ATGAGCATGATGATGGCCAGAAATGAA 888	

RESULT 5	Bg7411165	955 bp	mRNA	linear	EST 15-MAY-2001
LOCUS	Bg7411165	602631843p1	NCI_CGAP_Skn3	Homo sapiens	cDNA clone IMAGE:4776971 5',
DEFINITION	Bg7411165	RNA sequence.			
ACCESSION	Bg7411165				
VERSION	Bg7411165.1	GI:14051818			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 955)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc.				

CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM10630 row: f column: 12
High quality sequence stop: 805.

FEATURES
source
Location/Qualifiers
1..955

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4776971"
/clone_lib="NCI CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site: 1: Not:
Site: 2: Salt: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI-CGAP library."
BASE COUNT 233 a 210 c 275 g 237 t
ORIGIN

Query Match 42.4% Score 850.4; DB 12; Length 955;
Best Local Similarity 95.8%; Pred. No. 3.4e-211;
Matches 895; Conservative 0; Mismatches 36; Indels 3; Gaps 2;
QY 215 GCGCTGCTAGTGTCTGACCTGAAGCAGCGGCGGCGCGCTGCGGCTGTGTG 274
DB 1 GCGCTGCTAGTGTCTGACCTGAAGCAGCGGCGGCGCGCTGCGGCTGTGTG 60
QY 275 CAAAGCGGTGATGTCTGTCTGACCGCTTCCGCGGCTGTCTGATGAGAACTCCAGCT 334
DB 61 CAAAGCGGTGATGTCTGTCTGACCGCTTCCGCGGCTGTCTGATGAGAACTCCAGCT 120
QY 335 GGGCCAGAGATTTGACAGCGGGAATTCAGAGCTTATTTATCCAGGCTGATGATGAT 394
DB 121 GGGCCAGAGATTTGACAGCGGGAATTCAGAGCTTATTTATCCAGGCTGATGATGAT 180
QY 395 TGGCAGTGAAGACCTTCTGCGGTTAGTGTGCGCAGATATCACTATTGGCTTGTGTC 454
DB 181 TGGCAGTGAAGACCTTCTGCGGTTAGTGTGCGCAGATATCACTATTGGCTTGTGTC 240
QY 455 AGGTGTCTCTCAAAATTTGACAGAGTGTGAGATCCGTATGCCCGCTGATCTCTCT 514
DB 241 AGGTGTCTCTCAAAATTTGACAGAGTGTGAGATCCGTATGCCCGCTGATCTCTCT 300
QY 515 GGGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 574
DB 301 GGGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360
QY 575 CCGCAGACGACTGGCAGAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 634
DB 361 CCGCAGACGACTGGCAGAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 420
QY 635 TTTAAGTCTTTTCTGTGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 694
DB 421 TTTAAGTCTTTTCTGTGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 480
QY 695 GAACATGTTGATGTGAGAGCCTTTCTATAGCACTTACAGACAGCAGATGGGAAT 754
DB 481 GAACATGTTGATGTGAGAGCCTTTCTATAGCACTTACAGACAGCAGATGGGAAT 540
QY 755 CATGGCTGTGAGAGCAATAGAACCCAGTCTTACAGAGCTGTGATCAAGAGCTTGGACT 814
DB 541 CATGGCTGTGAGAGCAATAGAACCCAGTCTTACAGAGCTGTGATCAAGAGCTTGGACT 600
QY 815 AAAGTGTGATGATTTCCCAATCAGATGAGATGATGATGATGATGATGATGATGATGAT 874
DB 601 AAAGTGTGATGATTTCCCAATCAGATGAGATGATGATGATGATGATGATGATGATGAT 660
QY 875 GTTGGAGATGATTTGCAAG 934
DB 661 GTTGGAGATGATTTGCAAG 720

QY 935 AGATGCTGTGTGACTCCGCTTGTGACTTTTGTGAGAGAGTGTTCATCATGATCAACAA 994
DB 721 AGATGCTGTGTGACTCCGCTTGTGACTTTTGTGAGAGAGTGTTCATCATGATCAACAA 780
QY 995 GGAACGGGCTGTTTATCACCAGTGAAGAGCAGAGC-GTGAAGCCCGCCCTGCACCTC 1053
DB 781 GGAACGGG--CTGCTTATCACCAGTGAAGAGCAGAGCAGAGAGCCCGCCCTGCACCTC 838
QY 1054 TGCCTTAAACACCCAGCAGATCCCTTTTCAAAAGAGGATCTTTCATAGAGAACCA 1113
DB 839 GGTGTGTTAAACCCAGCAGATCCCTTTTCAAAAGAGGATCTTTCATAGAGAACCA 898
QY 1114 CTGAGGAGATCTTGAAGATTTGATTCAGCCG 1147
DB 899 CTGAGGAGATCTTGAAGATTTGATTCAGCCG 932

RESULT 6
AL555978
LOCUS
DEFINITION AL555978 LTI_NFL006.PL2 Homo sapiens CDNA clone CS0DK010Y11 5
ACCESSION AL555978
VERSION AL555978.1 GI:12898227
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 873)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

FEATURES
source
Location/Qualifiers
1..873
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DK010Y11"
/clone_lib="LTI_NFL006.PL2"
/tissue="placenta"
/note="Vector: pCMVSPORT 6; Site: 1: Not; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: liang@lifestech.com URL:
<http://fulllength.invitrogen.com> 3 others

BASE COUNT 180 a 208 c 278 g 204 t
ORIGIN
Query Match 42.2% Score 846.2; DB 9; Length 873;
Best Local Similarity 99.3%; Pred. No. 4.1e-210;
Matches 867; Conservative 3; Mismatches 1; Indels 2; Gaps 2;
QY 4 CAGGCTGTGGGCTGAAGGCTGCTCAGTTCTTCAACGGGGGACTGGGA-AGC 62
DB 1 CAGGCTGTGGGCTGAAGGCTGCTCAGTTCTTCAACGGGGGACTGGGA-AGC 60
QY 63 GCGATGACACTGAGAGGATCTCGGTGTGAGCTGTGCGGCTGGCCCGGCGCCGCTTC 122
DB 61 GCGATGACACTGAGAGGATCTCGGTGTGAGCTGTGCGGCTGGCCCGGCGCCGCTTC 120
QY 123 TGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
DB 121 TGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

```

QY 183 CGTAGAGCTGAGCCGCTTGGCCGGGGCAAGCGCTGCTAGTGTGACCTGGAACAG 242
    |||
    |||
    |||
Db 181 CGGTACACCTGAGCCCTTGGCCGGGGCAAGCGCTGCTAGTGTGACCTGGAACAG 240
QY 243 CCGGGGGAGCCCGCGCTGCGCGCTGTGCAAGGGGTGCGATGTGCTGTGAGACCC 302
    |||
    |||
    |||
Db 241 CCGGGGGAGCCCGCGCTGCGCGCTGTGCAAGGGGTGCGATGTGCTGTGAGACCC 300
QY 303 TTCCGCGCGGTGTCATGAGAAACTCCACCTGGGCCCAAGATTTGCAAGCGGGAAT 362
    |||
    |||
    |||
Db 301 TTCCGCGCGGTGTCATGAGAAACTCCACCTGGGCCCAAGATTTGCAAGCGGGAAT 360
QY 363 CCAAGGCTTATTAATGCAAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTCCGGGTTA 422
    |||
    |||
    |||
Db 361 CCAAGGCTTATTAATGCAAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTCCGGGTTA 420
QY 423 GGTGGCCAGATATCAACTTTTGGCTTGTCTGAGTGTCTCTCAAAAATTTGGAGAGT 482
    |||
    |||
    |||
Db 421 GGTGGCCAGATATCAACTTTTGGCTTGTCTGAGTGTCTCTCAAAAATTTGGAGAGT 480
QY 483 GGTGAGATCCGTATGCCCCGCTGAATCTCTGCTGACTTTGCTGGTGGCTTATG 542
    |||
    |||
    |||
Db 481 GGTGAGATCCGTATGCCCCGCTGAATCTCTGCTGACTTTGCTGGTGGCTTATG 540
QY 543 TGTGCACTGGGCAT-TATTAATGCTCTTTTGAACCGACACGACTGGCAAGGCTCAGT 601
    |||
    |||
    |||
Db 541 TGTGCACTGGGCAT-TATTAATGCTCTTTTGAACCGACACGACTGGCAAGGCTCAGT 600
QY 602 CATGATGCAATATGTTGGAAGAACAGATATTTAAGTCTTCTGTGGAAGAACTCA 661
    |||
    |||
    |||
Db 601 CATGATGCAATATGTTGGAAGAACAGATATTTAAGTCTTCTGTGGAAGAACTCA 660
QY 662 GAATGAGTCTGTGGGAACACCTCGAGAGACAAACATTTGGATGGTGGAGACCTTT 721
    |||
    |||
    |||
Db 661 GAATGAGTCTGTGGGAACACCTCGAGAGACAAACATTTGGATGGTGGAGACCTTT 720
QY 722 CTATGACACTTACAGACAGACAGATGGGAATTCATGCTGTGGAGCAATAGAACCCA 781
    |||
    |||
    |||
Db 721 CTATGACACTTACAGACAGACAGATGGGAATTCATGCTGTGGAGCAATAGAACCCA 780
QY 782 GTTCTAGACCTGCTGTCAAGAGACTTGAGTAAAGTGTGATGAATCTCCCATCAGT 841
    |||
    |||
    |||
Db 781 GTTCTAGACCTGCTGTCAAGAGACTTGAGTAAAGTGTGATGAATCTCCCATCAGT 840
QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAA 874
    |||
    |||
    |||
Db 841 GAGCATGATGATTTGGCCAGAAATGAAGAA 873

RESULT 7
ALS71115/c 838 bp mRNA linear EST 16-FEB-2001
LOCUS ALS71115 LYL_NFL006.PL2 Homo sapiens cDNA clone CS0D1027YJ12 3
DEFINITION prime, mRNA sequence.
ACCESSION ALS71115
VERSION ALS71115.1 GI:12928089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
            Genoscope-Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
            1. 838
FEATURES
            source
            /organism="Homo sapiens"
            /db_xref="taxon:9606"

```

```

/clone="CS0D1027YJ12"
/clone_lib="LYL_NFL006.PL2"
/tissue_type="placenta"
/note="Vector: PCWVSPORT 6; Site: 1; NotI: 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCWVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 236 a 181 c 152 g 265 t 4 others
ORIGIN

Query Match 41.2%; Score 826.2; DB 9; Length 838;
Best Local Similarity 98.8%; Pred. No. 6.9e-205;
Matches 828; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 726 ACGACTTACAGACAGAGATGGGAATTCATGCTGTGGAGCAATGAAACCCAGTTC 785
    |||
    |||
    |||
Db 838 ACAACTACAGAAACAGAAATGGGAATTCATGCTGTGGAGCAATGAAACCCAGTTC 779
QY 786 TACGAGCTGCTGATCAAGAAGCTTGAAGTGTGATGAACCTCCCAATCAGATGAGC 845
    |||
    |||
    |||
Db 778 TACGAGCTGCTGATCAAGAAGCTTGAAGTGTGATGAACCTCCCAATCAGATGAGC 719
QY 846 ATGATGATTTGGCCAGAAATGAAGAAAGTTCGCAATGTTGCAAAAGAGCAG 905
    |||
    |||
    |||
Db 718 ATGATGATTTGGCCAGAAATGAAGAAAGTTCGCAATGTTGCAAAAGAGCAG 659
QY 906 GCAGAGTGTGTCAAAATCTTTGACGCGCAGATGCCGTGTGACTCCGTTTGTACTTT 965
    |||
    |||
    |||
Db 658 GCAGAGTGTGTCAAAATCTTTGACGCGCAGATGCCGTGTGACTCCGTTTGTACTTT 599
QY 966 GAGAGGTTTTCATCATCATGATCACACACAGAAAGGGGCTGTTTATCACAGTGAAG 1025
    |||
    |||
    |||
Db 598 GAGAGGTTTTCATCATCATGATCACACACAGAAAGGGGCTGTTTATCACAGTGAAG 539
QY 1026 CAGAGAGTGAAGCCCGCCCGCCGACCTCTGCTGTTAAACACCCAGCATCCCTTCTTC 1085
    |||
    |||
    |||
Db 538 CAGAGAGTGAAGCCCGCCCGCCGACCTCTGCTGTTAAACACCCAGCATCCCTTCTTC 479
QY 1086 AAAAGGATCTTTTCATAGAGAAACACATGAGAGATGACTTGAAGATTTGGATTGAGC 1145
    |||
    |||
    |||
Db 478 AAAAGGATCTTTTCATAGAGAAACACATGAGAGATGACTTGAAGATTTGGATTGAGC 419
QY 1146 CCGGAAGAGATTTATCAGCTTAACTGATGATTAATCATTTGAAGTATTAAGTAAAGCT 1205
    |||
    |||
    |||
Db 418 CCGGAAGAGATTTATCAGCTTAACTGATGATTAATCATTTGAAGTATTAAGTAAAGCT 359
QY 1206 AGTCTTAACTTCCAGAGCCCGCAGCTCAAGTGAATTTGAATGATGCTTTTACAGTGA 1265
    |||
    |||
    |||
Db 358 AGTCTTAACTTCCAGAGCCCGCAGCTCAAGTGAATTTGAATGATGCTTTTACAGTGA 299
QY 1266 GTAACACATTAACATTTGATGATGAGAAACATGAGAGAACATTTACAGTGTCTTACAC 1325
    |||
    |||
    |||
Db 298 GTAACACATTAACATTTGATGATGAGAAACATGAGAGAACATTTACAGTGTCTTACAC 239
QY 1326 TCTAATCAAGAAAGATTTACAGACTGTGATTTACAGTATGATGATTTTACAAATG 1385
    |||
    |||
    |||
Db 238 TCTAATCAAGAAAGATTTACAGACTGTGATTTACAGTATGATGATTTTACAAATG 179
QY 1386 GTTATCATTTAGGGCTTTGATTTATTAACATTTGGGACTTATTAATTAATGATGAT 1445
    |||
    |||
    |||
Db 178 GTTATCATTTAGGGCTTTGATTTATTAACATTTGGGACTTATTAATTAATGATGAT 119
QY 1446 ATTCTGCTTCCAGATTTGCTGATATATTTGTTGATATTAAGATTTCTTGAATATATTT 1505
    |||
    |||
    |||
Db 118 ATTCTGCTTCCAGATTTGCTGATATATTTGTTGATATTAAGATTTCTTGAATATATTT 59
QY 1506 GAATGGTCTTACTGAAAAAGAAATGATATATTTCTTGAACACATCCATATACATTTAT 1563

```

```

Db      58  GAATGGGTCTAGTGAATAAAGATATATATCTTGAAGACATGATATACATTAT 1
|||||
RESULT 8
AL551698                                842 bp  mRNA  linear  EST 16-FEB-2001
LOCUS      AL551698 LTI_NFL006_P12 Homo sapiens cDNA clone CS0D1062YP05 5
DEFINITION prime, mRNA sequence.
ACCESSION  AL551698
VERSION     AL551698.1 GI:12889898
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 842) Jesse, J. and Polayes, D.
AUTHORS   Li, W. B., Gruber, C., Gruber, C., Gruber, C., Gruber, C., Gruber, C.,
TITLE     Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    Contact: Genoscope
            Genoscope Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
    source
        1..842
        Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="CS0D1062YP05"
            /clone_id="LTI_NFL006_P12"
            /tissue="placenta"
            /note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA
            was primed with a NotI-oligo(dT) primer. Five prime end
            enriched, double-stranded cDNA was digested with Not I and
            cloned into the Not I and Eco RV sites of the pCMVSPORT 6
            vector. Library was normalized. Library was constructed by
            Life Technologies. Contact : Peng Liang Life Technologies,
            a division of Invitrogen 9800 Medical Center Drive
            Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
            Email : lliang@lifetech.com URL :
            http://fulllength.invitrogen.com"

BASE COUNT  189 a 197 c 247 g 198 t 11 others
ORIGIN
Query Match 40 7% Score 815.8; DB: 9; Length 842;
-Best Local Similarity 97.9% Pred. No. 3,6e-202;
Matches 825; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

Oy      63  GCCATGGCAGTGCAGGCGATCTGGTGTGAGCTTCCGGCTGGCCGGCGCTTC 122
|||||
Db      1  GCCATGGCAGTGCAGGCGATCTGGTGTGAGCTTCCGGCTGGCCGGCGCTTC 60
|||||
Oy      123 TGTGTATGTGCTGTGCTGACTTGGGGCGCGTGTGTACGGGTGAGCCGGCGCTCC 182
|||||
Db      61 TGTGTATGTGCTGTGCTGACTTGGGGCGCGTGTGTACGGGTGAGCCGGCGCTCC 120
|||||
Oy      183 CGCTACGAGTGAAGCCGTTGGCCGGGCAAGCGTCCGTAGTGTGAGCTGAACAG 242
|||||
Db      121 CGCTACGAGTGAAGCCGTTGGCCGGGCAAGCGTCCGTAGTGTGAGCTGAACAG 180
|||||
Oy      243 CGCGGGGAGCGCGCGTCTCGGCGCTGTGTCAACCGGTGCGATGTCTCTGAGACCC 302
|||||
Db      181 CGCGGGGAGCGCGCGTCTCGGCGCTGTGTCAACCGGTGCGATGTCTCTGAGACCC 240
|||||
Oy      303 TTCCGGCGGGGTGCATGAGAAACTGCACGTGGCGCCAGATTTCTGACAGGGAAAT 362
|||||
Db      241 TTCCGGCGGGGTGCATGAGAAACTGCACGTGGCGCCAGATTTCTGACAGGGAAAT 300
|||||
Oy      363 CCAAGCTTATTTATGACAGGCTGAGTTTGGCCACTGAGGAAGCTTCTGCGCGTTA 422
|||||
Db      301 CCAAGCTTATTTATGACAGGCTGAGTTTGGCCACTGAGGAAGCTTCTGCGCGTTA 360
|||||
Oy      423 GCTGGCCAGATATCACTATTGGCTTGTGTGACGTGTCTCTCAAAAATTGCGAGAAT 482
|||||

Db      361 GGTGGCCAGATATCACTATTGGCTTGTGTGACGTGTCTCTCAAAAATTGCGAGAAT 420
|||||
Oy      483 GGTGAGAAATCCGTATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGCTTATG 542
|||||
Db      421 GGTGAGAAATCCGTATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGCTTATG 480
|||||
Oy      543 TGTGACAGGCGCATTAATGAGCTTTTGTGACCGCACAGCAGTGCAGAGGCTCAGT 602
|||||
Db      481 TGTGACAGGCGCATTAATGAGCTTTTGTGACCGCACAGCAGTGCAGAGGCTCAGT 540
|||||
Oy      603 ATTGAATGCAATATGTTGGAAGAGACAGATATTAAGTCTTTCTGTGGAACCTAG 662
|||||
Db      541 ATTGAATGCAATATGTTGGAAGAGACAGATATTAAGTCTTTCTGTGGAACCTAG 600
|||||
Oy      663 AATGAGCTGTGTGGGAAGACACCTGAGAGCAACATGTTGATGAGTGCAGACCTTC 722
|||||
Db      601 AATGAGCTGTGTGGGAAGACACCTGAGAGCAACATGTTGATGAGTGCAGACCTTC 660
|||||
Oy      723 TATGAGCTTACAGGACAGCATGATGGGAATTCATGCTGTTGGCAATGACCCAG 782
|||||
Db      661 TATGAGCTTACAGGACAGCATGATGGGAATTCATGCTGTTGGCAATGACCCAG 720
|||||
Oy      783 TTCTACGAGCTGCTGATCAAGAAGACTTGAATGATGATGAATCCCATCAGATG 842
|||||
Db      721 TTCTACGAGCTGCTGATCAAGAAGACTTGAATGATGATGAATCCCATCAGATG 780
|||||
Oy      843 ACCATGATGATTTGGCCAGAAATGAAGAGATTTGCGAGATGATTTGCAAGAGACG 902
|||||
Db      781 ACCATGATGATTTGGCCAGAAATGAAGAGATTTGCGAGATGATTTGCAAGAGAG 839
|||||
Oy      903 AAG 905
|||||
Db      840 AAG 842

RESULT 9
BM723657                                823 bp  mRNA  linear  EST 01-MAR-2002
LOCUS      BM723657
DEFINITION UI-E-EJ0-a1q-n-09-0-UI_r1 UI-E-EJ0 Homo sapiens cDNA clone
ACCESSION  BM723657
VERSION     BM723657.1 GI:19044988
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 823)
AUTHORS   Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL    Genome Res. 6 (9), 791-806 (1996)
MEDLINE    9704447
COMMENT    Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel.: 319 335 8250.
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
            Location/Qualifiers
                1..823
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="UI-E-EJ0-a1q-n-09-0-UI"

```

```

/cclone_lib="UI-E-E30"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
choroid"
/dev_stage="fetal and adult"
/lab_host="PH10B (Life Technologies) (71 phage resistant)"
/notes="Organ: eye; Vector: pRT73-Pac (pharmacia) with a
modified polylinker; Site: 1: EcoR I; Site: 2: Not I;
UI-E-E30 is a subtracted cDNA library constructed
according to Bonaldi, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pRT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterior segment, AATGCCCAT;
optic nerve, CCATTAGTGT; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
```

BASE COUNT 249 a 136 c 191 g 224 t 3 others

Query Match 40.6%; Score 813.6; DB 14; Length 823;
Best local Similarity 99.1%; Pred. No. 1.4e-201;
Matches 816; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

OY 660 CAGAAATCAGCTCTGTGGAGACCTCGAGACAGAACATGTTGGTGGACACCT 719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 CAGAAATGAGCTGTGGAGACCTCGAGACAGAACATGTTGGTGGAGACCT 60
OY 720 TTCTATACGATCAGAGAGAGAGATGGGATTTGCTGTGGAGAGATGAAGACC 779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 TTCTATACGATCAGAGAGAGAGATGGGATTTGCTGTGGAGAGATGAAGACC 120
OY 780 CAGTTCTACGAGCTGCTGATCAAGAGACTTGAAGTCTGATGAAGTCTCCCATCAG 839
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 CAGTTCTACGAGCTGCTGATCAAGAGACTTGAAGTCTGATGAAGTCTCCCATCAG 180
OY 840 ATAGCATGATGATGATGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCAAGAG 899
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 ATAGCATGATGATGATGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCAAGAG 240
OY 900 ACAGAGCAGAGTGTGTCAATCTTTGAGGAGACAGATGCTGTGACTCCGGTCTG 959
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 ACAGAGCAGAGTGTGTCAATCTTTGAGGAGACAGATGCTGTGACTCCGGTCTG 300
OY 960 ACTTTTGAGGAGTGTGTCAATCTTTGAGGAGACAGATGCTGTGACTCCGGTCTG 1019
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 ACTTTTGAGGAGTGTGTCAATCTTTGAGGAGACAGATGCTGTGACTCCGGTCTG 360
OY 1020 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
OY 1080 TCTTTTAAAGGAGATCTTTGATAGGAGACAGACTGAGAGATTTGAAAGATTTGGA 1139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 TCTTTTAAAGGAGATCTTTGATAGGAGACAGACTGAGAGATTTGAAAGATTTGGA 480
OY 1140 TTCAGCGCGAAGAGATTTATCAGCTTAACTAGATTTAAATCTTGAAGTAAAGTGA 1199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 TTCAGCGCGAAGAGATTTATCAGCTTAACTAGATTTAAATCTTGAAGTAAAGTGA 540
OY 1200 AAAGCTAGTCTTAACTTCCAGGCGCAGGCTCAAGGATTTGAATTCGATTTACAG 1259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 541 AAAGCTAGTCTTAACTTCCAGGCGCAGGCTCAAGGATTTGAATTCGATTTACAG 600
OY 1260 TGTAGAGTAAACATTAATTTATGATGAGAAACATGAGAGAAAGTATTAAAGTGTCC 1319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 601 TGTAGAGTAAACATTAATTTATGATGAGAAACATGAGAGAAAGTATTAAAGTGTCC 660
```

```

OY 1320 TACCACCTTAATCAAGAAAGATTAACAGACTGATCTGATCTACAGTGTGATGAATCTTA 1379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 661 TACCACCTTAATCAAGAAAGATTAACAGACTGATCTGATCTACAGTGTGATGAATCTTA 720
OY 1380 AAAATGGTTATTCATTTAGGCGCTTTGATTTTAAAACTTTGGTACTTAAATTAATG 1439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 721 AAAATGGTTATTCATTTAGGCGCTTTGATTTTAAAACTTTGGTACTTAAATTAATG 780
OY 1440 GTAGTTATTCCTGCTCCACTTTCCTGATATATTTGTTGATA 1482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 781 GTAGTTATTCCTGCTCCACTTTCCTGATATATTTGTTGATA 823

RESULT 10
AK002401
LOCUS
DEFINITION:
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Mus musculus
clone:0610009H21.
Mus musculus (strain: C57BL/6J) adult male kidney cDNA to mRNA,
clone_lib=RIKEN full-length enriched mouse cDNA library
AK002401
AK002401.1 GI:12832356
HTC; CAP trapper.
Mus musculus (strain: C57BL/6J) adult male kidney cDNA to mRNA,
clone_lib=RIKEN full-length enriched mouse cDNA library
clone:0610009H21.

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsui, M.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system -384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuenli, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Stauch, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Botfield, D., Bojunga, N.,
Carninci, P., de Bonaldi, M.F., Brownstein, M.J., Bul, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, I., Storch, K.F., Suzuki, H.,
```


Db 857 AAGCAGATGCTCCAGATTTTGGACGGACAGATGCTGTGACCCAGTGTACG 916
 QY 963 TTGTAGAGAGTTGTTCATCATGATCAGACAGAGAGAGGGGCTGTATTCACAGTGA 1022
 Db 917 TTGTAGAGAGGGCCCTCCACACACAGACAGAGAGGGGCTGTATTCACAGTGA 976
 QY 1023 GAGCAGACGTCGACCCCGCCCTGACCTTGTCTTTAAACACCCAGCCATCCCTT 1082
 Db 977 GAGCAGCTCCCGACCCCGCCCTGACCTTGTCTTTAAACACCCAGCCATCCCT 1036
 QY 1083 TTCAAAGGAGTCTTTCATCATGAGACACACTGAGAGACTGTGAAGATTTGATTC 1142
 Db 1037 GCCAAAAGGAGCCCTTCTGTAGGGAGACACCGTAGAAGTCTTACAGATATGATTC 1096
 QY 1143 AGCCGCGAGAGATTTATCAGCTTACTCAGATAAATCATTTGAAGTAATAGATAA 1202
 Db 1097 AGTCAGAGAGATCTTTCACCTGACCTCAGATAGAAATCGTTGAAGTAAAGATAA 1156
 QY 1203 GCTAGCTCTACTTCCAGGCGCCAGCTCAAGTGAATTTGAATACCTGATTTACAGT 1282
 Db 1157 GCCAATCTCTGACT - CAGGCTTATAGCTCAAGAACTGAAGGCTGCACTCCACTGG 1214
 QY 1263 AGAGTAACATATCATTTGATTCATGAGAAACATGAGAGACAGATATACAGT - GTCC 1321
 Db 1215 GGAGAGATGCCCAATTTGTGTATGAAATGTGATGAAACAGCAATGAAGTATCCAA 1274
 QY 1322 CCACTTATCAGAAAAGAAATACAGACTCTGATTTCTACAGTATGATTAATTCATA 1381
 Db 1275 ATATCCCAATCAGATCCCAAGAAAGGCTGTTACAGATATGATTCGCGCTTACGCT 1334
 QY 1382 AATGGTATCATTTAGGGCTTTGATTTATTAACCTTGGTACTATCTAAATTAAGGT 1441
 Db 1335 GCTATATCAGAGCTCTGTGTATGAGAAATTTGTGTGTGATGATGATGATGATGATG 1394
 QY 1442 AGTATTTCTGCTTCCAGATTTGATTTGATTTATTTGATTTGATTTGATTTGATTTA 1501
 Db 1395 AGCT - TTCTGCTTTCAGTTCCTTGGTGAAGTGTATCCATTTATTAACCCCTTTATA 1453
 QY 1502 TTTTGAA 1508
 Db 1454 AATACAA 1460

RESULT 11
 LOCUS AL545355 824 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL545355 LTI_NFL006_PL2 Homo sapiens cDNA clone CS01027YJ12 5
 prime, mRNA sequence.
 ACCESSION AL545355
 VERSION AL545355.1 GI:12877836
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 824)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segrel@genoscope.cns.fr, web : www.genoscope.cns.fr.
 FEATURES
 source
 1..824
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS01027YJ12"
 /clone_lib="LTI_NFL006_PL2"
 /issue_type="placenta"
 /note="Vector: PCWSPORT 6; site: 1; NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the PCWSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com

BASE COUNT 176 a 191 c 257 g 198 t 2 others
 ORIGIN
 Query Match 39.7%; Score 796.4; DB 9; Length 824;
 Best Local Similarity 99.2%; Pred. No. 4.3e-197;
 Matches 819; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

QY 71 ACTCAGGAGATCTCGGTGAGAGCTGTCCGGCTGCCCCGGCCGTTCTGTGCTAT 130
 Db 1 ACTCAGGAGATCTCGGTGAGAGCTGTCCGGCTGCCCCGGCCGTTCTGTGCTAT 60
 QY 131 GGTCTGCTGACTTCCGGGCGCGTGTGATACGGTGGACCGCCGGCTCCCTACGA 190
 Db 61 GGTCTGCTGACTTCCGGGCGCGTGTGATACGGTGGACCGCCGGCTCCCTACGA 120
 QY 191 CGTGAGCGGCTTGGGCGGCGGCAAGCGCTGCTAGTGTGAGCTGAAGACAGCGCGGG 250
 Db 121 CGTGAGCGGCTTGGGCGGCGGCAAGCGCTGCTAGTGTGAGCTGAAGACAGCGCGGG 180
 QY 251 AGCCGCGGTGCGGCGTGTGCAAGCGGTGATGTGCTGGAAGCCCTTCCGCG 310
 Db 181 AGCCGCGGTGCGGCGTGTGCAAGCGGTGATGTGCTGGAAGCCCTTCCGCG 240
 QY 311 CGGTGTATGAGAACTCCAGCTGGGCGCCAGATTTCTGAGGGGAAATCCAAAGCT 370
 Db 241 CGGTGTATGAGAACTCCAGCTGGGCGCCAGATTTCTGAGGGGAAATCCAAAGCT 300
 QY 371 TATTTATGCCAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 430
 Db 301 TATTTATGCCAGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 360
 QY 431 CGATATCACTATTTGGCTTTGTCAGGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAA 490
 Db 361 CGATATCACTATTTGGCTTTGTCAGGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAA 420
 QY 491 TCCGATGCGCCCGCTGATCTCCGGCTGATTTGGTGGTGGTGGTGGTGGTGGTGGT 550
 Db 421 TCCGATGCGCCCGCTGATCTCCGGCTGATTTGGTGGTGGTGGTGGTGGTGGTGGT 480
 QY 551 GGGCATTATATGAGCTTTTGGACCGCACAGCACTGGCAAGGCTCAGTCAATTTGATGC 610
 Db 481 GGGCATTATATGAGCTTTTGGACCGCACAGCACTGGCAAGGCTCAGTCAATTTGATGC 540
 QY 611 AATATGCTGAGAGCAACAGATATTTAAGTCTTTTCTGTGAAATCTCAGAAATCGAG 670
 Db 541 AATATGCTGAGAGCAACAGATATTTAAGTCTTTTCTGTGAAATCTCAGAAATCGAG 600
 QY 671 TCTGTGGAGACACTCGAGAGCAACATGTTGATGTGTGAGACACTTCTATAGAG 730
 Db 601 TCTGTGGAGACACTCGAGAGCAACATGTTGATGTGTGAGACACTTCTATAGAG 659
 QY 731 TTACAGAGACAGATGGGGAATCATGGCTGTGGAGCAATATAGACCCAGTCTACGA 790
 Db 660 TTACAGAGACAGATGGGGAATCATGGCTGTGGAGCAATATAGACCCAGTCTACGA 718
 QY 791 GCTGCTGATCAAAAGACTTGGACTTAAGTGTGATGAATCCCAATCAGATGAGACATGA 850
 Db 719 GCTGCTGATCAAAAGACTTGGACTTAAGTGTGATGAATCCCAATCAGATGAGACATGA 778
 QY 851 TGATGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCGAAG 896
 Db 779 TGATGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTCGAAG 824

RESULT 12
 BQ962523


```

LOCUS      B0962523              890 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT.8817570 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6379327
ACCESSION  B0962523
VERSION     B0962523.1 GI:22378001
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 890)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgabbs-remail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LCM2566 row: c column: 08
             High quality sequence stop: 750.

FEATURES
     source
         1..890
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:6379327"
         /clone_1ib="NIH_MGC_42"
         /tissue_type="epithelioid carcinoma cell line"
         /lab_host="DH10B (phage-resistant)"
         /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
             Site_2: EcoRI; cDNA made by oligo-dT priming.
             Directionally cloned into EcoRI/XhoI sites using the
             following 5' adaptor: GGCAAGGAG(G). Size selected >500bp
             for average insert size 1.8kb. Library constructed by Ling
             Hong in the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies).
             Note: this is a NIH-MGC library."

BASE COUNT  187 a 221 c 278 g 203 t
ORIGIN
Query Match 39.0%; Score 781.8; DB 14; Length 890;
Best Local Similarity 99.1%; Pred. No. 2.9e-193;
Matches 786; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 24 AAGGCGTCGACGATTCTCTAGCGGGGCACTGGAGAGCCCATGCGACTGCGAGGCATC 83
DB 1 AAGGGCGTCAGATTCTCTAGCGGGGCACTGGAGAGCCCATGCGACTGCGAGGCATC 60
QY 84 TCGGTGTCGACCTGTCCGGGCTGGGCCCCGGGCGCTTGTGCTATGCTGCTGCTGAC 143
DB 61 TCGGTATGAGACTGTCCGGGCTGGGCCCCGGGCGCTTGTGCTATGCTGCTGCTGAC 120
QY 144 TTGGGGGGCGGTGTGTGACGCGTGGACCGCGCGCTCCGCTAGCAGCTGAGCCGCTTG 203
DB 121 TTGGGGGGCGGTGTGTGACGCGTGGACCGCGCGCTCCGCTAGCAGCTGAGCCGCTTG 180
QY 204 GGCGGGGGAAGCGCTCGCTAGTGTGACCTGAAGCAGCGCGGGAGCGCGCTGTG 263
DB 181 GGCGGGGGAAGCGCTCGCTAGTGTGACCTGAAGCAGCGCGGGAGCGCGCTGTG 240
QY 264 CGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGAGAGCCCTTCCGCGCGGTGTGAG 323
DB 241 CGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGAGAGCCCTTCCGCGCGGTGTGAG 300
QY 324 AAACCTCAGCTGGGCCAGAGATTCTGCAGCGGGGAAATCAAGGCTTATTATGCCAGG 383
DB 301 AAACCTCAGCTGGGCCAGAGATTCTGCAGCGGGGAAATCAAGGCTTATTATGCCAGG 360

```

```

QY 384 CTGAGTGGATTTGGCCAGTCAGAGAGCTTCTGCCGTTAGCTGGCCAGCATATCAACTAT 443
DB 381 CTGAGTGGATTTGGCCAGTCAGAGAGCTTCTGCCGTTAGCTGGCCAGCATATCAACTAT 420
QY 444 TTGGCTTTGTCAGAGTGTCTCTCAAAAATTTGGCAGAGTGGTGAAGTCCGTATGCCCG 503
DB 421 TTGGCTTTGTCAGAGTGTCTCTCAAAAATTTGGCAGAGTGGTGAAGTCCGTATGCCCG 480
QY 584 CTGAATCTCTGCTGCTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563
DB 481 CTGAATCTCTGCTGCTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 584 GCTCTTTTTCACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 623
DB 541 GCTCTTTTTCACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600
QY 624 GGAACACATATTTTAAGTCTTTCTGTGAGAAATCTGAGAAATCGAGTCTGTGGAGCA 683
DB 601 GGAACACATATTTTAAGTCTTTCTGTGAGAAATCTGAGAAATCGAGTCTGTGGAGCA 660
QY 684 CCTGAGAGCAGAAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 743
DB 661 CCTGAGAGCAGAAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 744 GATGGGAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803
DB 721 GATGGGAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 804 GCACTTGTGACTAA 816
DB 781 GGTCTGGGGAGAA 793

RESULT 13
LOCUS      B0941482              890 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT.8821476 Lupskl.sciatlc.nerve Homo sapiens cDNA clone
ACCESSION  B0941482
VERSION     B0941482.1 GI:22356960
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 890)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgabbs-remail.nih.gov
             Tissue Procurement: Dr. James R. Lupskl
             cDNA Library Preparation: Life Technologies, Inc.
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM13623 row: 1 column: 21
             High quality sequence stop: 621.

FEATURES
     source
         1..890
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:6203684"
         /clone_1ib="Lupskl.sciatlc.nerve"
         /sex="male"
         /tissue_type="sciatic nerve"
         /dev_stage="adult, 70 yr"
         /lab_host="DH10B"
         /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
             NotI; Site_2: SalI; cDNA made by oligo-dT priming.
             Directionally cloned using the following adaptors:

```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 22:36:28 ; Search time 686.574 Seconds
(Without alignments)
8263.356 Million cell updates/sec

Title: US-09-967-305-1

Perfect score: 2005

Sequence: 1 ttgcagctctgctggctggg.....acatccagaataaattctt 2005

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5019383 seqs, 1414814461 residues

Total number of hits satisfying chosen parameters: 10038766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_MA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
1	2003.4	99.9	2005	1	PCT-US02-24567-104
2	2003.4	99.9	2005	8	US-10-210-120-104
3	1950.8	97.3	2068	8	US-10-316-540-11
4	1616.8	80.6	2946	8	US-10-316-540-11
5	1574.2	78.5	1821	6	US-09-593-793A-107
6	1574.2	78.5	1821	8	US-10-294-025-107
7	1574.2	78.5	1821	8	US-10-294-025-107
8	1201.4	59.9	21814	8	US-10-129-909-107
9	830	41.4	1504	1	PCT-US03-03482-3147
10	830	41.4	1504	1	PCT-US03-03194-3149
11	830	41.4	1504	8	US-10-152-319A-1546
12	830	41.4	1504	8	US-10-301-856-852
13	830	41.4	1504	8	US-10-338-044-1802
14	830	41.4	1504	8	US-10-256-909-172
15	830	38.6	1504	9	US-60-436-643-3149
16	774.6	31.6	1464	8	US-10-144-771-6845
17	633.8	26.1	572	8	US-10-316-540-12
18	522.6	25.7	537	6	US-10-310-673-1859
19	515	25.7	537	6	US-09-593-793A-74
20	515	25.7	537	6	US-10-294-025-74
21	428.4	21.4	430	8	US-10-129-909-74
22	428.4	21.4	430	8	PCT-US02-34777-1504
23	428.4	21.4	430	8	US-10-283-017-1504
24	406.6	20.3	773	6	US-09-593-793A-3

c	25	406.6	20.3	773	8	US-10-294-025-3	Sequence 3, Appl1
c	26	406.6	20.3	773	8	US-10-129-909-3	Sequence 3, Appl1
c	27	403.2	20.1	793	6	US-09-593-793A-33	Sequence 33, Appl1
c	28	403.2	20.1	793	8	US-10-294-025-33	Sequence 33, Appl1
c	29	403.2	20.1	793	8	US-10-129-909-33	Sequence 33, Appl1
c	30	400.2	20.0	816	6	US-09-593-793A-2	Sequence 2, Appl1
c	31	400.2	20.0	816	8	US-10-294-025-2	Sequence 2, Appl1
c	32	400.2	20.0	816	8	US-10-129-909-2	Sequence 2, Appl1
c	33	351.6	19.5	601	5	US-09-947-907-5679	Sequence 5679, Ap
c	34	354.4	17.7	471	8	US-10-316-540-14	Sequence 14, Appl
c	35	316.2	15.8	601	5	US-09-947-907-5681	Sequence 5681, Ap
c	36	314.4	15.7	386	6	US-09-513-999C-3525	Sequence 3525, Ap
c	37	305.6	15.2	335	6	US-10-310-673-1093	Sequence 1093, Ap
c	38	290	14.5	301	6	US-09-593-793A-242	Sequence 242, App
c	39	290	14.5	301	6	US-10-294-025-242	Sequence 242, App
c	40	290	14.5	301	8	US-10-129-909-242	Sequence 242, App
c	41	289	14.4	301	6	US-09-593-793A-252	Sequence 252, App
c	42	289	14.4	301	8	US-10-294-025-252	Sequence 252, App
c	43	289	14.4	301	8	US-10-129-909-252	Sequence 252, App
c	44	283.4	14.1	510	6	US-09-912-293-165626	Sequence 165626,
c	45	262	13.1	264	6	US-09-912-293-108124	Sequence 108124,

ALIGNMENTS

RESULT 1
PCT-US02-24567-104
Sequence 104, Application PC/TUS0224567
GENERAL INFORMATION:
APPLICANT: Chinaiyan, Arul M.
APPLICANT: Rubin, Mark A.
TITLE OR INVENTION: Expression Profile of Prostate Cancer
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: PCT/US02/24567
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
SEQ ID NO 104
LENGTH: 2005
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-24567-104

Query Match 99.9% Score 2003.4; DB 1: Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTGCAGCTCTCTGGCTGGGCTTAAGGCTCTCAGTTTCCTTCACGGGCGACTGGGAA 60
DB 1 TTGCAGCTCTCTGGCTGGGCTTAAGGCTCTCAGTTTCCTTCACGGGCGACTGGGAA 60
OY 61 GCGGCATGCGACATGCGAGGATCTGCTGAGAGCTGTCGGGCTGGGCGGCGCT 120
DB 61 GCGGCATGCGACATGCGAGGATCTGCTGAGAGCTGTCGGGCTGGGCGGCGCT 120
OY 121 TCTGTGATGTCGTCGCTGACTTCGCGGCGCTGTGATGACGCTGAGCCGCGGCT 180
DB 121 TCTGTGATGTCGTCGCTGACTTCGCGGCGCTGTGATGACGCTGAGCCGCGGCT 180
OY 181 CCCGCTGACGACGCGGCTGGGCGGCGGCGGCGGCGGCTGAGTGTGAGCGTGAAGC 240
DB 181 CCCGCTGACGACGCGGCTGGGCGGCGGCGGCGGCGGCTGAGTGTGAGCGTGAAGC 240
OY 241 AGCGCGGAGCGCGGCTGTCGCGGCTGTCGCAAGCGGCGGCGGCGGCGGCGGCG 300
DB 241 AGCGCGGAGCGCGGCTGTCGCGGCTGTCGCAAGCGGCGGCGGCGGCGGCGGCG 300

```

QY 301 CTTCCGCCGCGGTGTCATGAGAAACTCAGCTGGGCCAGAGATCTGCGCGGAAA 360
    |||
Db 301 CCTTCCGCCGCGGTGTCATGAGAAACTCAGCTGGGCCAGAGATCTGCGCGGAAA 360
QY 361 ATCCAGGCTATTATATCCAGGCTGAGTGTGGCCATCGAGAGCTTCGCCGT 420
    |||
Db 361 ATCCAGGCTATTATATCCAGGCTGAGTGTGGCCATCGAGAGCTTCGCCGT 420
QY 421 TAGCTGGCCAGATATCAACTATTTGGCTTGTGAGGTGTTCTCCCAAAATTTGGCAGAA 480
    |||
Db 421 TAGCTGGCCAGATATCAACTATTTGGCTTGTGAGGTGTTCTCCCAAAATTTGGCAGAA 480
QY 481 GTGGTGAATCCGTATGCCCCGCTGAATCTCTGCTGCTGACTTGTCTGCTGCTGCTGCT 540
    |||
Db 481 GTGGTGAATCCGTATGCCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TGTGGCAGTGGGCAATTAATGGCTTTTGTACCCGACAGCCAGTGGCAAGGCTCAG 600
    |||
Db 541 TGTGGCAGTGGGCAATTAATGGCTTTTGTACCCGACAGCCAGTGGCAAGGCTCAG 600
QY 601 TCATTGATGCAAAATATGTTGGAGAACAGCATATTTAAGTCTTTTCTGTGAAAATCTC 660
    |||
Db 601 TCATTGATGCAAAATATGTTGGAGAACAGCATATTTAAGTCTTTTCTGTGAAAATCTC 660
QY 661 AGAATGAGTCTGTGGAGACACCTCGAGACAGACATCTGGATGGTGGAGACCTT 720
    |||
Db 661 AGAATGAGTCTGTGGAGACACCTCGAGACAGACATCTGGATGGTGGAGACCTT 720
QY 721 TCTATGACACTTACAGGACAGACAGATGGGGAATTCATGCTGTTGGACATAGAACCC 780
    |||
Db 721 TCTATGACACTTACAGGACAGACAGATGGGGAATTCATGCTGTTGGACATAGAACCC 780
QY 781 AGTTCTACGAGCTCTGATCAAAAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGA 840
    |||
Db 781 AGTTCTACGAGCTCTGATCAAAAGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGA 840
QY 841 TGACATGAGATGATGGCCAGAAATGAAGAAGATTTGCAAGATATTTGCAAAAGAA 900
    |||
Db 841 TGACATGAGATGATGGCCAGAAATGAAGAAGATTTGCAAGATATTTGCAAAAGAA 900
QY 901 CGAAGGAGAGTGTGTCAAATCTTTGACGGCAGACAGATCCTGTGTGACTCGGTTCTGA 960
    |||
Db 901 CGAAGGAGAGTGTGTCAAATCTTTGACGGCAGACAGATCCTGTGTGACTCGGTTCTGA 960
QY 961 CTTTGTAGGAGGTGTTTCATCATATCAACAAGAAAGGCGCTGTTATACCACTG 1020
    |||
Db 961 CTTTGTAGGAGGTGTTTCATCATATCAACAAGAAAGGCGCTGTTATACCACTG 1020
QY 1021 AGGAGGAGAGTGTAGCCCCCGCTGACCTGTGCTGTTAAACACCCCAACCATCCCTT 1080
    |||
Db 1021 AGGAGGAGAGTGTAGCCCCCGCTGACCTGTGCTGTTAAACACCCCAACCATCCCTT 1080
QY 1081 CTTTCAAAAGGATCTTTCTATAGAGAACACACTGAGAGATCTTAAAAATTTGGAT 1140
    |||
Db 1081 CTTTCAAAAGGATCTTTCTATAGAGAACACACTGAGAGATCTTAAAAATTTGGAT 1140
QY 1141 TCAGCCCCGGAAGATTATCAGCTTAACAGATTAATCAATTTGAAGATTAAGGTTAA 1200
    |||
Db 1141 TCAGCCCCGGAAGATTATCAGCTTAACAGATTAATCAATTTGAAGATTAAGGTTAA 1200
QY 1201 AAGCTAGTCTTAACTTCCAGGCCCCGAGGCTCAAGTGAATTTGAATCTGATTTACGT 1260
    |||
Db 1201 AAGCTAGTCTTAACTTCCAGGCCCCGAGGCTCAAGTGAATTTGAATCTGATTTACGT 1260
QY 1261 GTAGAGTACACATTAATGATGATGAAACATGAGAGACAGTATTCAGTGCTT 1320
    |||
Db 1261 GTAGAGTACACATTAATGATGATGAAACATGAGAGACAGTATTCAGTGCTT 1320
QY 1321 ACCACTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATTTCAA 1380
    |||
Db 1321 ACCACTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATTTCAA 1380
QY 1381 AAATGTTATCATTAAGGCTTTTGAATTTAATAAATTTGGTACTTATTAATTAATG 1440
    |||

```

```

Db 1381 AAATGTTATCATTAAGGCTTTTGAATTTAATAAATTTGGTACTTATTAATTAATG 1440
QY 1441 TAGTATATCTGCTCCATCCAGTGTGCTGATATATTTGATATTAAGATTTCTGACTAT 1500
    |||
Db 1441 TAGTATATCTGCTCCATCCAGTGTGCTGATATATTTGATATTAAGATTTCTGACTAT 1500
QY 1501 ATTTGAATGGGTCTTACTGAAAGAATGATATATTTCTTGAAGACATGATATACAT 1560
    |||
Db 1501 ATTTGAATGGGTCTTACTGAAAGAATGATATATTTCTTGAAGACATGATATACAT 1560
QY 1561 TATTTACACTCTTATTTTACAAATGTAAGAAATGAGAAAGCCCAAAATTTGATGGGA 1620
    |||
Db 1561 TATTTACACTCTTATTTTACAAATGTAAGAAATGAGAAAGCCCAAAATTTGATGGGA 1620
QY 1621 TAAAGTACGTTGAATGATGATGTTGCTATCCAGGCTTTTGTGCTGCTGCTGCTGCT 1680
    |||
Db 1621 TAAAGTACGTTGAATGATGATGTTGCTATCCAGGCTTTTGTGCTGCTGCTGCTGCT 1680
QY 1681 ATCTCCCTCTAAGCACATTTCCAACTTTAGCAAGATTAACACTTTGTAATTTGCAAA 1740
    |||
Db 1681 ATCTCCCTCTAAGCACATTTCCAACTTTAGCAAGATTAACACTTTGTAATTTGCAAA 1740
QY 1741 GAAAAGTTTCACTGTATTTGAATCAAGATGCTTCAACTGAAAAAACAATATCAAAATA 1800
    |||
Db 1741 GAAAAGTTTCACTGTATTTGAATCAAGATGCTTCAACTGAAAAAACAATATCAAAATA 1800
QY 1801 ATGAGAAATGTTGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
    |||
Db 1801 ATGAGAAATGTTGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CTGATATCAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
    |||
Db 1861 CTGATATCAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1921 CTCATGTTGTTGATTTCTCTCAGGCTGATGAGAGTTCGATATACCAACACA 1980
    |||
Db 1921 CTCATGTTGTTGATTTCTCTCAGGCTGATGAGAGTTCGATATACCAACACA 1980
QY 1981 CAGCAATCCAGAAATTAAGTTCT 2005
    |||
Db 1981 CAGCAATCCAGAAATTAAGTTCT 2005

RESULT 2
US-10-210-104
: Sequence 104, Application us/10210120
: GENERAL INFORMATION:
: APPLICANT: Chinaiyan, Arul M.
: APPLICANT: Streekumar, Arun.
: TITLE OF INVENTION: Expression Profile of Prostate Cancer
: FILE REFERENCE: UM-07221
: CURRENT APPLICATION NUMBER: us/10/210,120
: CURRENT FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: US 60/309,581
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: US 60/334,468
: PRIOR FILING DATE: 2001-11-15
: NUMBER OF SEQ ID NOS: 123
: SOFTWARE: Patent version 3.2
: SEQ ID NO 104
: LENGTH: 2005
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-210-104

Query Match          99.9%; Score 2003.4; DB 8; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
|||||

```

Db 1 TTGCAAGCTGCTGGGCTGGGCTGAAGGGCTGCTACGTTTCCTTCAAGCGGGGCATGAGGAA 60
 QY 61 GCGCATGGCAGCTGAGAGGAGCATCTCGGTGTGAGAGCTGTCCGGCTGGCCCGCCGCGCT 120
 Db 61 GCGCATGGCAGCTGAGAGGAGCATCTCGGTGTGAGAGCTGTCCGGCTGGCCCGCCGCGCT 120
 QY 121 TCTGTCTATGAGTCTGAGCTGATCTGAGGAGGAGCTGTGAGTACGAGGAGCGGCGGCT 180
 Db 121 TCTGTCTATGAGTCTGAGCTGATCTGAGGAGGAGCTGTGAGTACGAGGAGCGGCGGCT 180
 QY 181 CCGGCTACGAGTGAAGCGCTTGGGCGGGGCAAGGCGCTGCTGAGTGTGAGCTGAGAGC 240
 Db 181 CCGGCTACGAGTGAAGCGCTTGGGCGGGGCAAGGCGCTGCTGAGTGTGAGCTGAGAGC 240
 QY 241 AGCGGGGAGAGCGGCGCTTGGGCGGGGCAAGGCGCTGCTGAGTGTGAGCTGAGAGC 300
 Db 241 AGCGGGGAGAGCGGCGCTTGGGCGGGGCAAGGCGCTGCTGAGTGTGAGCTGAGAGC 300
 QY 301 CTTTCCGCGGCTGTCAATGAGAACTCCAGCTGGGCGGAGATTTGACGCGGAGAA 360
 Db 301 CTTTCCGCGGCTGTCAATGAGAACTCCAGCTGGGCGGAGATTTGACGCGGAGAA 360
 QY 361 ATCCAAGCTTATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGAACTTCTCCGCT 420
 Db 361 ATCCAAGCTTATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGAACTTCTCCGCT 420
 QY 421 TAGCTGGCCAGATATCAACTATTTGGCTTGTGAGAGTGTCTCTCAAAATTTGACAGAA 480
 Db 421 TAGCTGGCCAGATATCAACTATTTGGCTTGTGAGAGTGTCTCTCAAAATTTGACAGAA 480
 QY 481 GTGTGAGAGTCCGTATGCGGCGGAGATCCCTGGCTGATCTTGGTGGTGGCTTGA 540
 Db 481 GTGTGAGAGTCCGTATGCGGCGGAGATCCCTGGCTGATCTTGGTGGTGGCTTGA 540
 QY 541 TGTGTGACGAGGCAATTAATGCTCTTTTGAACGCAACAGCACTGGCAAGGCTGAG 600
 Db 541 TGTGTGACGAGGCAATTAATGCTCTTTTGAACGCAACAGCACTGGCAAGGCTGAG 600
 QY 601 TCAATGATGCAAAATGAGTGTGAGAGAGAGATTTTAACTTTTCTGTGTGAAAGCTC 660
 Db 601 TCAATGATGCAAAATGAGTGTGAGAGAGAGATTTTAACTTTTCTGTGTGAAAGCTC 660
 QY 661 AGAAATCGAGTCTGTGGGAGAGCACTGAGAGCAGAAATGTTGATGATGATGAGCAGCTT 720
 Db 661 AGAAATCGAGTCTGTGGGAGAGCACTGAGAGCAGAAATGTTGATGATGATGAGCAGCTT 720
 QY 721 TCTATACGACTTACAGAGCAGAGAGAGAGATTCATGCTGTTGGAGCAATGAAGCC 780
 Db 721 TCTATACGACTTACAGAGCAGAGAGAGAGATTCATGCTGTTGGAGCAATGAAGCC 780
 QY 781 AGTTCTACAGAGTGTGATCAAAAGAGCTTGAAGTGTGATGAAGTCTCCCAATCAGA 840
 Db 781 AGTTCTACAGAGTGTGATCAAAAGAGCTTGAAGTGTGATGAAGTCTCCCAATCAGA 840
 QY 841 TGAGCATGATGATGGCCAGAAATGAAGAAGATTTGAGATGTATTTGCAAAAGAGA 900
 Db 841 TGAGCATGATGATGGCCAGAAATGAAGAAGATTTGAGATGTATTTGCAAAAGAGA 900
 QY 901 CGAAGGCAAGTGTGATCAAAATCTTTGAGGAGAGATGCTGTGATGATGATGATGATG 960
 Db 901 CGAAGGCAAGTGTGATCAAAATCTTTGAGGAGAGATGCTGTGATGATGATGATGATG 960
 QY 961 CTTTGAAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 Db 961 CTTTGAAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1021 AGAGCAGAGAGTGAAGCCCGCCCTGACCTGCTGCTTAAACACCCAGCAGCTT 1080
 Db 1021 AGAGCAGAGAGTGAAGCCCGCCCTGACCTGCTGCTTAAACACCCAGCAGCTT 1080
 QY 1081 CTTTCAAAAGGATCTTTCAATAGAGAGAGAGAGAGAGATTTGAAGATTTGGAT 1140
 Db 1081 CTTTCAAAAGGATCTTTCAATAGAGAGAGAGAGAGATTTGAAGATTTGGAT 1140

QY 1141 TCAGCCGGAAGAGATTTATCAGTTAACTCAGATAAATCATTTGAAGTAA 1200
 Db 1141 TCAGCCGGAAGAGATTTATCAGTTAACTCAGATAAATCATTTGAAGTAA 1200
 QY 1201 AAGCTATCTCTTAACTTCCAGGCGGCTCAAGTGAATTTGAATACGATTTACAGT 1260
 Db 1201 AAGCTATCTCTTAACTTCCAGGCGGCTCAAGTGAATTTGAATACGATTTACAGT 1260
 QY 1261 GTAGATGACATTAATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 1320
 Db 1261 GTAGATGACATTAATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 1320
 QY 1321 ACCACTTAATCAAGAAAGATTTACAGACTGTATTTCAAGTATGATTAATTTCA 1380
 Db 1321 ACCACTTAATCAAGAAAGATTTACAGACTGTATTTCAAGTATGATTAATTTCA 1380
 QY 1381 AATGATGATTAATGAGGCTTTGATTTATAAACTTGGGCTATATATCTAAATTTATG 1440
 Db 1381 AATGATGATTAATGAGGCTTTGATTTATAAACTTGGGCTATATATCTAAATTTATG 1440
 QY 1441 TAGTATTTCTGCTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1441 TAGTATTTCTGCTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1501 ATTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATGATATACAT 1560
 Db 1501 ATTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATGATATACAT 1560
 QY 1561 TATTTACACTTGTATTTACAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 Db 1561 TATTTACACTTGTATTTACAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 QY 1621 TAAAGTACAGTAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 TAAAGTACAGTAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 ATCTCCCTTACAGCATTTCCAACTTTAGCAACAGTATTTACACTTTGTAATTTGCAA 1740
 Db 1681 ATCTCCCTTACAGCATTTCCAACTTTAGCAACAGTATTTACACTTTGTAATTTGCAA 1740
 QY 1741 GAAAGTTTCACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
 Db 1741 GAAAGTTTCACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
 QY 1801 ATGAGAAATGTTGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATG 1860
 Db 1801 ATGAGAAATGTTGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATG 1860
 QY 1861 CTGATACAGTAACTGCGGCGCTGTTCCCGTGGGCTGCTGCGGCTGCTGAGCTTCTTT 1920
 Db 1861 CTGATACAGTAACTGCGGCGCTGTTCCCGTGGGCTGCTGCGGCTGCTGAGCTTCTTT 1920
 QY 1921 CTCATGTTGATTTCTCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATG 1980
 Db 1921 CTCATGTTGATTTCTCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATG 1980
 QY 1981 CAGCAATCCAGAAATTAAGTTCT 2005
 Db 1981 CAGCAATCCAGAAATTAAGATCT 2005

RESULT 3
 US-10-316-540-11
 ; Sequence 11, Application US/10316540
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenneth W. Doble
 ; TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
 ; FILE REFERENCE: RTS-0471
 ; CURRENT APPLICATION NUMBER: US/10/316,540
 ; CURRENT FILING DATE: 2002-12-10
 ; NUMBER OF SEQ ID NOS: 156

SEQ ID NO 11
LENGTH: 2068
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 143
OTHER INFORMATION: unknown
FEATURE:
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (89)...(1237)
US-10-316-540-11

Query Match Best Local Similarity 97.3%; Score 1950.8; DB 8; Length 2068;
Matches 1985; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

QY 1 TTGCAGGCTGCTGGGCTGGGCTGAAGGCTGCTCAGTTCTTCACGCGGGCACTGGGAA 60
DB 24 TTGCAGGCTGCTGGGCTGGGCTGAAGGCTGCTCAGTTCTTCACGCGGGCACTGGGAA 83
QY 61 GCGCCATGGCAGTGCAGGGGATCTGGTGGAGTGTCCGGCTGGGCGCGGGCCGCT 120
DB 84 GCGCCATGGCAGTGCAGGGGATCTGGTGGAGTGTCCGGCTGGGCGCGGGCCGCT 143
QY 121 TCTGTGCTATGTCCTGGCTGAGCTTCGGGGCGGCTGTGTACGCTGTGACCGGCGCGCT 180
DB 144 TCTGTGCTATGTCCTGGCTGAGCTTCGGGGCGGCTGTGTGTACGCTGTGACCGGCGCGCT 203
QY 181 CCGGCTACGAGCTGAGCGGCTGGGCGGGGCAAGCGCTGCTAGTCTGAGCTGAGC 240
DB 204 CCGGCTACGAGCTGAGCGGCTGGGCGGGGCAAGCGCTGCTAGTCTGAGCTGAGC 263
QY 241 AGCGGCGGGAGCGCGGCTGCTGGGCTGTGTGCAAGCGGCTGAGTGTGCTGTGAGC 300
DB 264 AGCGGCGGG--AGCGGCTGCTGGGCTGTGTGCAAGCGGCTGAGTGTGCTGTGAGC 321
QY 301 CCTTCGCGCGGCTGTGTGAGGAAACTCCAGCTGGGCGGCAAGATTCAGCGGGA 360
DB 322 CCTTCGCGCGGCTGTGTGAGGAAACTCCAGCTGGGCGGCAAGATTCAGCGGGA 381
QY 361 ATCCAAAGCTTATTTATGCGAGCTGAGTGAATTTGGCCAGT--CAGGAAGCTTTCGCG 418
DB 382 ATCCAAAGCTTATTTATGCGAGCTGAGTGAATTTGGCCAGT--CAGGAAGCTTTCGCG 441
QY 419 GTTAGCTGGCAGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAG 478
DB 442 GTTAGCTGGCAGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAG 501
QY 479 AAGTGTGAGAAATCGTATGCCCGCTGAATCTCTGGCTGAGCTTGGCTGGTGGCT 538
DB 502 AAGTGTGAGAAATCGTATGCCCGCTGAATCTCTGGCTGAGCTTGGCTGGTGGCT 561
QY 539 TATGTGTGACTGGGCTATTAATGGCTTTTGTACCGCAGCAGCTGGCAAGGCTCA 558
DB 562 TATGTGTGACTGGGCTATTAATGGCTTTTGTACCGCAGCAGCTGGCAAGGCTCA 621
QY 599 GGCATTTGATGCAAAATATGTTGGAAGGAAACAGATATTTAAGTCTTTTGTGGAAG 658
DB 622 GGCATTTGATGCAAAATATGTTGGAAGGAAACAGATATTTAAGTCTTTTGTGGAAG 681
QY 659 TCAGAAATCGAGTCTGTGGAGACACCTCGAGAGCAGAAACATGTTGATGTTGAGCACC 718
DB 682 TCAGAAATCGAGTCTGTGGAGACACCTCGAGAGCAGAAACATGTTGATGTTGAGCACC 741
QY 719 TTTCTATACGACTTACAGCAGCAGATGGGAAATTCAGTGTGTGAGCAATAGAAC 778
DB 742 TTTCTATACGACTTACAGCAGCAGATGGGAAATTCAGTGTGTGAGCAATAGAAC 801
QY 779 CAGGTCTACGAGCTGTGATCAAGAGCTTGAAGTAAATCTGAGCAATTTCCCAATCA 838
|||||

DB 802 CCAATTCTACGAGCTGCTGTATCAAAAGACTTGGACATTAAGTCTGATGAACTTCCCAATCA 861
QY 839 GATGAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTTCAAGAA 898
DB 862 GATGAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTTCAAGAA 921
QY 899 GACGAGGAGAGTGTGTCTAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCT 958
DB 922 GACGAGGAGAGTGTGTCTAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCT 981
QY 959 GACTTTTGAAGAGTTTTCATGATGATCAACAAGGAAGGGGCTGTTTATCACAG 1018
DB 982 GACTTTTGAAGAGTTTTCATGATGATCAACAAGGAAGGGGCTGTTTATCACAG 1041
QY 1019 TGAGAGCAGAGCTGAGCCCGCCCGCTGACCTGTCTGTTAAACCCAGCCATCC 1078
DB 1042 TGAGAGCAGAGCTGAGCCCGCCCGCTGACCTGTCTGTTAAACCCAGCCATCC 1101
QY 1079 TTCTTTCAAAAGGATCTTTTCAATAGAGAACACTGAGAGATATCTGAAATTTGG 1138
DB 1102 TTCTTTCAAAAGGATCTTTTCAATAGAGAACACTGAGAGATATCTGAAATTTGG 1161
QY 1139 ATTACGCGGAGAGATTTATCAGCTTAATCAGATTAATGATGAAGTAATAGT 1198
DB 1162 ATTACGCGGAGAGATTTATCAGCTTAATCAGATTAATGATGAAGTAATAGT 1221
QY 1199 AAAAGTAGTCTCTAACCTTCAGGCGCCAGGCTCAAGGTGAATTTGATCTGATTTACA 1258
DB 1222 AAAAGTAGTCTCTAACCTTCAGGCGCCAGGCTCAAGGTGAATTTGATCTGATTTACA 1281
QY 1259 GTGTAGAGTACACATTAATGTTATGATGAGGAAACATGAGGAGACAGTTCAGTGTGC 1318
DB 1282 GTGTAGAGTACACATTAATGTTATGATGAGGAAACATGAGGAGACAGTTCAGTGTGC 1341
QY 1319 CTACACTCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTATGATGATTTCT 1378
DB 1342 CTACACTCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTATGATGATTTCT 1401
QY 1379 AAAATGTTATATCATTAAGGCTTTGATTTATAAACTTGGTACTTATATTAATAT 1438
DB 1402 AAAATGTTATATCATTAAGGCTTTGATTTATAAACTTGGTACTTATATTAATAT 1461
QY 1439 GGTAGTATCTGCTTCCAGTGTGCTGATATATTTGTTGATTAAGTTCCTGACT 1498
DB 1462 GGTAGTATCTGCTTCCAGTGTGCTGATATATTTGTTGATTAAGTTCCTGACT 1521
QY 1499 ATATTTGAATGGGCTCTAGTGAAGAAAGATATATTTCTTGAAGACATTCGATATACA 1558
DB 1522 ATATTTGAATGGGCTCTAGTGAAGAAAGATATATTTCTTGAAGACATTCGATATACA 1581
QY 1559 TTTATTTACACTCTGATTTCTACATGTAGAAATGAGAAATGCCAAATTTGTATGCT 1618
DB 1582 TTTATTTACACTCTGATTTCTACATGTAGAAATGAGAAATGCCAAATTTGTATGCT 1641
QY 1619 GATTAAGTACGTTGAAGAAAGATGATTTGGTTCATTCAGAGCTTGTCTGGTGTCA 1678
DB 1642 GATTAAGTACGTTGAAGAAAGATGATTTGGTTCATTCAGAGCTTGTCTGGTGTCA 1701
QY 1679 TGATCTCCCTTAAGCAGATTTCAAACTTTAGCAAGAGTATACACTTGTATTTGCA 1738
DB 1702 TGATCTCCCTTAAGCAGATTTCAAACTTTAGCAAGAGTATACACTTGTATTTGCA 1761
QY 1739 AAGAAAAGTTTACGCTGATATGAATGAGAAATGCTTCAACTGAAAAAATATTCACAAA 1798
DB 1762 AAGAAAAGTTTACGCTGATATGAATGAGAAATGCTTCAACTGAAAAAATATTCACAAA 1821
QY 1799 TAATGAGAAATGTGTTGGCTCACTACGTAAGTCCAGAGGAGCACTCAATTTAGGCT 1858
DB 1822 TAATGAGAAATGTGTTGGCTCACTACGTAAGTCCAGAGGAGCACTCAATTTAGGCT 1881
QY 1859 GCCTGTATCCAGTAACTCGGGGCTGTTTCCCGTGGGCTGCGGCTGACCTTTCT 1918
DB 1882 GCCTGTATCCAGTAACTCGGGGCTGTTTCCCGTGGGCTGCGGCTGACCTTTCT 1941
|||||

OY	1734	TTGCAAGAAGAAATTCACCTGATTGGAAATACAATAGCCTTCCAACTGAAAAAACAATTC	1793
Db	1520	TTCGAAGAAGAAAAGTTTACCCTGATTGTGAATCAGAAATGCCCTTCAACTGAAAAAAAAATATC	1579
OY	1794	CAAAATATATGAGCAAAATGTGTGGCTOACTAGTAGATGCACAGAGGACAGTCAAGTTTTA	1855
Db	1580	CAAAATATATGAGGAAAAGTTGTGGCTCACACTAGCATAGATCCAGAGGAGACAGTCAAGTTTTA	1633
OY	1854	GCGTGTCCTGATATCCACTAACCTCGGGGAGCCGTGTTCCCGTGGGTCCTCGGGCTGTACAGT	1913
Db	1640	GCGTGTCCTGATATCCACTAACCTCGGGGAGCCGTGTTCCCGTGGGTCCTCTGAGCTGTACAGT	1699
OY	1914	TTTCCTTTCTCCATGTGTGTTGATTTTCTCTCAGGCGTGGTAGCAAGTTTGGATCTTAATACC	1973
Db	1700	TTTCCTTTCTCCATGTGTGTTGATTTTCTCTCAGGCGTGGTAGCAAGTTTGGATCTTAATACC	1758
OY	1974	CAACACACAGCAACATCCACAATAAAGTTCT 2005	
Db	1760	CAACACACAGCAACATCCACAATAAAGATCT 1791	

RESULT 5

```

US-09-593-793A-107
: Sequence 107, Application US/09593793A
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqun
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Helper, William
: TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
: FILE REFERENCE: 210121.42715C15
: CURRENT APPLICATION NUMBER: US/09/593,793A
: CURRENT FILING DATE: 2000-06-13
: NUMBER OF SEQ ID NOS: 814
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 107
: LENGTH: 1621
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-593-793A-107

```

Query Match	78.5%;	Score 1574.2;	DB 6;	Length 1621;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1576;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0

QY	62	CGCATATGGCATATGAGGGGACATCTGGGTCGTGAGACTGTCCGGGCTGGGCCCCGGGCCGTT	124
Db	1	CGCCATATGGCATATGAGGGGACATCTGGGTCATATGAGACTGTCCGGGCTGGGCCCCGGGCCGTT	60
QY	122	CTGTGCTATATGCTCTCTGGGCTGACTTCCGGGGCGCGCTGTGTAGCGGTGGACCCGGGCCGGCTC	184
Db	61	CTGTGCTATATGCTCTCTGGGCTGACTTCCGGGGCGCGCTGTGTAGCGGTGGACCCGGGCCGGCTC	120
QY	182	CCGCTAGACACTAGACCGGCTTTGGGGCCGGGGGCAACCGCTTCCCTAATGCTGGAACTGAAAGCA	244
Db	121	CCGCTAGACACTAGACCGGCTTTGGGGCCGGGGGCAACCGCTTCCCTAATGCTGGAACTGAAAGCA	180
QY	242	GCCCGGGGGAGCCGCCCTGTGCTGGGGGCTCTGTGCAACGGTGGATATGCTGCTGGAGCC	304

Dp	181	GC	CGG	GGG	GAC	CCG	CCG	CGT	CGC	GGC	CTG	CTG	CGA	CAAC	CGG	CTG	CGA	TG	TG	CTG	CTG	GAG	CC	240
Qy	302	CTT	CCG	CCG	CGG	GTG	CTAT	GCA	GA	AA	ACT	CC	AG	CT	CG	CC	CA	G	A	CT	CC	CA	GA	361
Dp	241	CTT	CCG	CCG	CGG	GTG	CTAT	GCA	GA	AA	ACT	CC	AG	CT	CG	CC	CA	G	A	CT	CC	CA	GA	300
Qy	362	TTCA	AGG	CTT	TTT	ATG	CG	AG	GG	CG	AG	ATG	GG	CG	CA	CT	CG	AG	GA	AG	CTT	CG	CG	421
Dp	301	TTCA	AGG	CTT	TTT	ATG	CG	AG	GG	CG	AG	ATG	GG	CG	CA	CT	CG	AG	GA	AG	CTT	CG	CG	360
Qy	422	AG	CTG	GC	CA	CA	AT	AT	CA	CA	CT	AT	TT	TG	CT	CT	CA	AG	CT	CT	CA	AA	AT	481
Dp	361	AG	CTG	GC	CA	CA	AT	AT	CA	CA	CT	AT	TT	TG	CT	CT	CA	AG	CT	CT	CA	AA	AT	420
Qy	482	TG	TG	AG	AA	AT	CC	GT	AT	G	CC	CG	CT	GA	AT	CT	CT	GG	CT	GA	TT	CT	GG	541
Dp	421	TG	TG	AG	AA	AT	CC	GT	AT	G	CC	CG	CT	GA	AT	CT	CT	GG	CT	GA	TT	CT	GG	480
Qy	542	GT	GT	GC	ACT	GGG	CA	TT	AT	TG	GG	CT	CT	TT	TG	AC	CG	CA	CG	CA	CG	CA	AG	601
Dp	481	GT	GT	GC	ACT	GGG	CA	TT	AT	TG	GG	CT	CT	TT	TG	AC	CG	CA	CG	CA	CG	CA	AG	540
Qy	602	CAT	TG	AT	G	AT	AT	TG	G	GA	GA	AA	CA	AG	CA	AT	TT	TA	AG	TT	CT	TT	CT	661
Dp	541	CAT	TG	AT	G	AT	AT	TG	G	GA	GA	AA	CA	AG	CA	AT	TT	TA	AG	TT	CT	TT	CT	600
Qy	662	GA	AA	TC	GA	TC	GT	GG	GA	AG	CA	CC	TC	GA	GA	CA	GA	AA	CA	AT	TT	GG	AT	721
Dp	601	GA	AA	TC	GA	TC	GT	GG	GA	AG	CA	CC	TC	GA	GA	CA	GA	AA	CA	AT	TT	GG	AT	660
Qy	722	CT	AT	AT	CA	CT	TA	CA	AG	GA	CA	CA	AG	CA	AT	TG	GG	GA	AT	CT	AT	TG	GA	781
Dp	661	CT	AT	AT	CA	CT	TA	CA	AG	GA	CA	CA	AG	CA	AT	TG	GG	GA	AT	CT	AT	TG	GA	720
Qy	782	GTT	CT	AC	AG	CT	GG	CT	GA	TC	AA	AA	AG	CA	CT	TT	GA	AG	CA	CT	CC	CA	AT	841
Dp	721	GTT	CT	AC	AG	CT	GG	CT	GA	TC	AA	AA	AG	CA	CT	TT	GA	AG	CA	CT	CC	CA	AT	780
Qy	842	GAG	CA	TG	GA	TG	GG	CG	CA	GA	AA	TG	AA	GA	AG	AT	TT	GA	AT	TT	GC	AA	GA	901
Dp	781	GAG	CA	TG	GA	TG	GG	CG	CA	GA	AA	TG	AA	GA	AG	AT	TT	GA	AT	TT	GC	AA	GA	840
Qy	902	GA	AG	CA	GA	TG	GG	CG	CA	GA	AA	TG	AA	GA	AG	AT	TT	GA	AT	TT	GC	AA	GA	961
Dp	841	GA	AG	CA	GA	TG	GG	CG	CA	GA	AA	TG	AA	GA	AG	AT	TT	GA	AT	TT	GC	AA	GA	900
Qy	962	TTT	TG	AG	AG	AG	TTT	CT	AT	CA	TG	AT	CA	CA	CA	GA	AA	CG	GG	CG	CT	TT	AT	102
Dp	901	TTT	TG	AG	AG	AG	TTT	CT	AT	CA	TG	AT	CA	CA	CA	GA	AA	CG	GG	CG	CT	TT	AT	960
Qy	1022	GG	AG	CA	GA	AG	CT	GA	CC	CG	CG	CG	CT											

OY	1382	AAGGTATACATATGAGGCTTTGATTTATAAAGCTTGGACTTACTAAATATG	1441
Db	1321	AATGGTTACATTTAGGGCTTTGATTTATAAAGCTTGGACTTACTAAATATG	1380
OY	1442	AGTTATTCGGCTTCAGCTTGGTGTATATATTTGGTATATTAACATCTGACTATA	1501
Db	1381	AGTTATTCGGCTTCAGCTTGGTGTATATATTTGGTATATTAACATCTTGGACTATA	1440
OY	1502	TTTTGAATGGGCTTCTAGTAAAAAGAAATGATATATTTCTTGAAGACATGATATACATTT	1561
Db	1441	TTTTGAATGGGCTTCTAGTAAAAAGAAATGATATATTTCTTGAAGACATGATATACATTT	1500
OY	1562	ATTTACACTCTTGTATCTACATGTATGAATAATGAGAAATGCCACAAATTTATGTGAT	1621
Db	1501	ATTTACACTCTTGTATCTACAAATGTAGAAAATGAGAAATGCCACAAATTTATGTGAT	1560
OY	1622	AAAAGTCACGTGAACAAGA 1640	
Db	1561	AAAAGTCACGTGAACAAGA 1579	
RESULT 6			
US-10-294-025-107			
Sequence 107, Application US/10294025			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Stolk, John A.			
APPLICANT: Kalos, Michael D			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
FILE REFERENCE: 210121.427C29			
CURRENT APPLICATION NUMBER: US/10/294,025			
NUMBER OF SEQ ID NOS: 1038			
SOFTWARE: FASTSEQ for Windows Version 3.0			
SEQ ID NO 107			
LENGTH: 1621			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-294-025-107			
Query Match			
Best local similarity 78.5%; Score 1574.2; DB 8; Length 1621.			
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
OY	62	CGCATGAGCAGCAGGAGGATCGTGGTGGAGCTGCGGCGTGGCCCGGCGCGGT	121
Db	1	CGCATGAGCAGCAGGAGGATCGTGGTGGAGCTGCGGCGTGGCCCGGCGCGGT	60
OY	122	CTGTGCTATGCTCTGCGCTGACTTGGGGCGCGTGTGTACGCGGTGAGCCGGCGCTC	181
Db	61	CTGTGCTATGCTCTGCGCTGACTTGGGGCGCGTGTGTGTACGCGGTGAGCCGGCGCTC	120
OY	182	CGGCTACGAGCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGAGACTTAAGCA	241
Db	121	CGGCTACGAGCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGAGACTTAAGCA	180
OY	242	GCGCGGAGGAGCCCGCTGCTGGCGGCGTGTGCAACGCGTGCAGATGTCTCTGAGACC	301
Db	181	GCGCGGAGGAGCCCGCTGCTGGCGGCGTGTGCAACGCGTGCAGATGTCTCTGAGACC	240
OY	302	CTTCCGCGCGGCTGATGAGAGAAATCCAGCTGGGGCCAGAAATTTCTGCAGCGGAAAA	361
Db	241	CTTCCGCGCGGCTGATGAGAGAAATCCAGCTGGGGCCAGAAATTTCTGCAGCGGAAAA	300
OY	362	TCCAAAGCTTATTTATGCCAGGCTGAGTGTGATTTGGCACTCAGGAAGCTTCTGCGGGTT	421
Db	301	TCCAAAGCTTATTTATGCCAGGCTGAGTGTGATTTGGCACTCAGGAAGCTTCTGCGGGTT	360
OY	422	AGCTGGCCAGATATCACTATTTTGGCTTGTCAAGTGTCTCTCAAAAATTTGGCAGAG	481
Db	361	AGCTGGCCAGATATCACTATTTTGGCTTGTCAAGTGTCTCTCAAAAATTTGGCAGAG	420

[illegible]

QY	1562	ATTTCACGCTTGATTCATCAATGTAGAAAAGAGCAAAATGCCACAAATGTATGTGAT	1621
Db	1501	ATTTCACGCTTGATTCATCAATGTAGAAAATGAGAAATGCCACAAATGTATGTGAT	1560
QY	1622	AAAAGTCAGTGAACAGA 1640	
Db	1561	AAAAGTCAGTGAACAAA 1579	
RESULT 7			
US-10-129-909-107			
: Sequence 107, Application US/10129909			
: GENERAL INFORMATION:			
: APPLICANT: Corixa Corporation			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillion, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan Louise			
: APPLICANT: Jiang Yugu			
: APPLICANT: Reed, Steven G.			
: APPLICANT: Kalos, Michael			
: APPLICANT: Fanger, Gary			
: APPLICANT: Retter, Mark			
: APPLICANT: Solk, John			
: APPLICANT: Day, Craig			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Wang, Aljun			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
: FILE REFERENCE: 210121.42720PC			
: CURRENT APPLICATION NUMBER: US/10/129,909			
: CURRENT FILING DATE: 2000-11-09			
: NUMBER OF SEQ ID NOS: 531			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 107			
: LENGTH: 1621			
: TYPE: DNA			
: ORGANISM: Homo sapien			
US-10-129-909-107			
QY	62	CGCCATGGCAGTCAGGAGCATCTCGGTGTGGAGCTGTCCGGCCCGGCGCCGTT	121
Db	1	CGCCATGGCAGTCAGGAGCATCTCGGTGTGGAGCTGTCCGGCCCGGCGCCGTT	60
QY	122	CTGTGCTATGCTCGCGGTGACTTGGGGCGCGGTGTGATCCGTGAGACCGGCGCTC	181
Db	61	CTGTGCTATGCTCGCGGTGACTTGGGGCGCGGTGTGATCCGTGAGACCGGCGCTC	120
QY	182	CCGCTACGACGTGAGCCGCTTGGGCCGGGCGAAGCGCTCGTATGTGTGGACCTGAAGA	241
Db	121	CCGCTACGACGTGAGCCGCTTGGGGCGGAGCGCTCGTATGTGTGGACCTGAAGA	180
QY	242	GCCGGGGGAGCGCGGTGCTGCGGCTGCTGTGCAAGCGGTGGATGTCCTGTGAGCC	301
Db	181	GCCGGGGGAGCGCGGTGCTGCGGCTGCTGTGCAAGCGGTGGATGTCCTGTGAGCC	240
QY	302	CTTCCGCCCGGTGTGCATGAGAAAATCCAGCTGGGCCCAAGATTTGTGCAGCGGAAAA	361
Db	241	CTTCCGCCCGGTGTGCATGAGAAAATCCAGCTGGGCCCAAGATTTGTGCAGCGGAAAA	300
QY	362	TCCAAAGGCTTATTTATGCGCAGGCTGATGTGATTTGGCCAGTGAAGAGTTTGGCGGTT	421
Db	301	TCCAAAGGCTTATTTATGCGCAGGCTGATGTGATTTGGCCAGTGAAGAGTTTGGCGGTT	360
QY	422	AGCTGGCCACGATATCACTATTTGGCTTGTGACAGGTGTCTCTCAAAAATTTGGCAGAG	481
Db	361	AGCTGGCCACGATATCACTATTTGGCTTGTGACAGGTGTCTCTCAAAAATTTGGCAGAG	420
QY	482	TGGTGAATCCGTAATGCCCCGCTGAATCTCCCTGGCTGACTTGTGCTGTGATGACCTTAT	541

Db	421	TGTTGAGAGATCCGATATCCCGCGTGAATCTCGTGGCTACTTTGCGGGTGAGGCTTAT	480
Qy	542	GTGTGCACTGGGCATTATTAATGGCTCTTTTGTACCGCCACACGACACTGGCAGGGTCAAGT	601
Db	481	GTGTGCACTGGGCATTATTAATGGCTCTTTTGTACCGCCACACGACACTGGCAGGGTCAAGT	540
Qy	602	CATTGATGCAAAATATGGTGGAGAGAACAGCATATTAATACCTCTTTTGTGGAAAAATCA	661
Db	541	CATTGATGCAAAATATGGTGGAGAGAACAGCATATTAATACCTCTTTTGTGGAAAAATCA	600
Qy	662	GAATTCGAGTCTGTGGGAAGCACCTCGAGAGACGAACATGTTGGATGTTGGAGCACCTTT	721
Db	601	GAATTCGAGTCTGTGGGAAGCACCTCGAGAGACGAACATGTTGGATGTTGGAGCACCTTT	660
Qy	722	CTATACGACTTACAGGACACACAGATGGGGAATTCAAGCTGTGTGGAGCAATGAAACCCCA	781
Db	661	CTATACGACTTACAGGACACACAGATGGGGAATTCAAGCTGTGTGGAGCAATGAAACCCCA	720
Qy	782	GTCTTACGAGCTGCTGTATCCAAAGAGCTTGGACTTAAAGTCTGTATGTAACCTTCCCAATCAGAT	841
Db	721	GTCTTACGAGCTGCTGTATCCAAAGAGCTTGGACTTAAAGTCTGTATGTAACCTTCCCAATCAGAT	780
Qy	842	GAGCATGATGATTTGGCCACAAATGGAAGAAAGTTTCAGATGATTTTGGCAAAACAACAC	901
Db	781	GAGCATGATGATTTGGCCACAAATGGAAGAAAGTTTTCAGATGATTTTGGCAAAACAACAC	840
Qy	902	GAAGGACAGAGTGGTGTCAAAATCTTTGACGGCACAGATGGCTGTGTACCTCGGTCTGTAC	961
Db	841	GAAGGACAGAGTGGTGTCAAAATCTTTGACGGCACAGATGGCTGTGTACCTCGGTCTGTAC	900
Qy	962	TTTTGAGAGAGTGTGTATATCATGATCACAACAAGAACGGGCTGTTTATACCAATGTA	1021
Db	901	TTTTGAGAGAGTGTGTATATCATGATCACAACAAGAACGGGCTGTTTATACCAATGTA	960
Qy	1022	GGAGCAGAGAGTGTAGCCCGCCCGCTGACCTCGTGTAAACACCCCGACCATCCCTTC	1081
Db	961	GGAGCAGAGAGTGTAGCCCGCCCGCTGACCTCGTGTAAACACCCCGACCATCCCTTC	1020
Qy	1082	TTTCAAAAAGGAGTCTTTTCATATAGAGAACACACTGAGAGATACTTGAAGAAATTTGGATT	1141
Db	1021	TTTCAAAAAGGAGTCTTTTCATATAGAGAACACACTGAGAGATACTTGAAGAAATTTGGATT	1080
Qy	1142	CAGCGCGGAAGAGTTTATATAGCTTAACTCAGTAAATCATTTGAAAGTAATACAGTAAA	1201
Db	1081	CAGCGCGGAAGAGTTTATATAGCTTAACTCAGTAAATCATTTGAAAGTAATACAGTAAA	1140
Qy	1202	AGCTAGTCTCTAACTTCCAGGCCCCAGGGCTCAAGTAAATTTAATACCTGCATTTCACGTG	1261
Db	1141	AGCTAGTCTCTAACTTCCAGGCCCCAGGGCTCAAGTAAATTTAATACCTGCATTTCACGTG	1200
Qy	1262	TAGAGTAAACATATACATTTGTATATGATGGAAACATGGAGAACATGATTAACAGTCTCCTA	1321
Db	1201	TAGAGTAAACATATACATTTGTATATGATGGAAACATGGAGAACATGATTAACAGTCTCCTA	1260
Qy	1322	CCACTCTAATCAAGAAAAAGAAATTAACAGACTCTGATTCCTACAGTGAATGATTAATCTCTAAA	1381
Db	1261	CCACTCTAATCAAGAAAAAGAAATTAACAGACTCTGATTCCTACAGTGAATGATTAATCTCTAAA	1320
Qy	1382	AATGGTATATCAATAGGGCTTTTGAATTTATAAAACCTTTGGGTACTTACTAAATATATGTT	1441
Db	1321	AATGGTATATCAATAGGGCTTTTGAATTTATAAAACCTTTGGGTACTTACTAAATATATGTT	1380
Qy	1442	AGTATTTCTGCTCCCAAGTGTGCTGATATATTTGTTGATATTAAGATTTCTGACTCTATA	1501
Db	1381	AGTATTTCTGCTCCCAAGTGTGCTGATATATTTGTTGATATTAAGATTTCTGACTCTATA	1440
Qy	1502	TTTTGAATGGGTTCTACTAGTAAAAAGAAAGATATATCTTGTGAAGACATGATATACATTT	1561
Db	1441	TTTTGAATGGGTTCTACTAGTAAAAAGAAAGATATATCTTGTGAAGACATGATATACATTT	1500
Qy	1562	ATTTTACACTCTGATTTCTACATATGTAGAAATGAGAAATGCCACAAATGTGATGTGAT	1621

Db 1501 ATTACACTGTGATCTACATGTAAGAAATGAGAAATGCCAAATGTATGTGAT 1560
 Qy 1622 AAAAGTCAGTGAACAGAGA 1640
 |||||||
 Db 1561 AAAAGTCAGTGAACAGAGA 1579

RESULT 8

US-10-316-540-4
 : Sequence 4, Application US/10316540
 : GENERAL INFORMATION:
 : APPLICANT: Kenneth W. Dobie
 : APPLICANT: Ravi Jain
 : TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
 : FILE REFERENCE: RFS-0471
 : CURRENT APPLICATION NUMBER: US/10/316,540
 : CURRENT FILING DATE: 2002-12-10
 : NUMBER OF SEQ ID NOS: 156
 : SEQ ID NO 4
 : LENGTH: 21814
 : TYPE: DNA
 : ORGANISM: H. sapiens
 : FEATURE:
 US-10-316-540-4

Query Match 59.9%; Score 1201.4; DB 8; Length 21814;
 Best Local Similarity 99.9%; Pred. No. 5e-287;
 Matches 1202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 803 AGGACTGTGACCTAAAGCTGTGTAAGTCCCATCATGATGACATGATGATGGCCAGA 862
 |||||||
 Db 19084 AGGACTGTGACCTAAAGCTGTGTAAGTCCCATCATGATGACATGATGATGGCCAGA 19143
 Qy 863 AATGAAGAAGAGTTTGCAGTGTATTTGCAAGAAAGCAAGAGCGAGTGTCTCAAT 922
 |||||||
 Db 19144 AATGAAGAAGAGTTTGCAGTGTATTTGCAAGAAAGCAAGAGCGAGTGTCTCAAT 19203
 Qy 923 CTTTGACGGACAGATGCTGTGTGACTCCGTTCTGACTTTTGAGAGGTTTTCATCA 982
 |||||||
 Db 19204 CTTTGACGGACAGATGCTGTGTGACTCCGTTCTGACTTTTGAGAGGTTTTCATCA 19263
 Qy 983 TGATCAACAAGAGAAAGGGGCTGTTTATCACCACTGAGAGAGAGCGTGAAGCCCCG 1042
 |||||||
 Db 19264 TGATCAACAAGAGAAAGGGGCTGTTTATCACCACTGAGAGAGAGCGTGAAGCCCCG 19323
 Qy 1043 CCTGACACTCTGCTGTAAACACCCAGCCATCCCTTTTCAAAAGGATCCCTTCAT 1102
 |||||||
 Db 19324 CCTGACACTCTGCTGTAAACACCCAGCCATCCCTTTTCAAAAGGATCCCTTCAT 19383
 Qy 1103 AGGAGAACACACTGAGGATGATCTGAAAGATTGGATTACAGCCGGAAGATTTATCA 1162
 |||||||
 Db 19384 AGGAGAACACACTGAGGATGATCTGAAAGATTGGATTACAGCCGGAAGATTTATCA 19443
 Qy 1163 GCTTAACCTCAATTAATCATTTGAAGTAAATAGGTAAAGCTAGTCTTAACTCCAGG 1222
 |||||||
 Db 19444 GCTTAACCTCAATTAATCATTTGAAGTAAATAGGTAAAGCTAGTCTTAACTCCAGG 19503
 Qy 1223 CCCAGGCTCAAGTATTTGAATGATGCTGATTTTACAGTGTAGATGATACATTAACATTTGT 1282
 |||||||
 Db 19504 CCCAGGCTCAAGTATTTGAATGATGCTGATTTTACAGTGTAGATGATTAACATTAACATTTGT 19563
 Qy 1283 ATGCATGGAACATGAGGAAGACAGTATTTACAGTGTCTACACTCTAATCAAGAAAGAA 1342
 |||||||
 Db 19564 ATGCATGGAACATGAGGAAGACAGTATTTACAGTGTCTACACTCTAATCAAGAAAGAA 19623
 Qy 1343 TTACAGACTGTGATCTACAGTGTGATTTGAATTTCTAATAAGTGTATTCATTTAGGCTTT 1402
 |||||||
 Db 19624 TTACAGACTGTGATCTACAGTGTGATTTGAATTTCTAATAAGTGTATTCATTTAGGCTTT 19683
 Qy 1403 TGATTTATTAACCTTTGGGTACTATATCTAATTAATGATGATTTAGCTTCCAGTTT 1462
 |||||||
 Db 19684 TGATTTATTAACCTTTGGGTACTATATCTAATTAATGATGATTTAGCTTCCAGTTT 19743

Qy 1463 GCTTGATATATTTGTTGATTAATTAAGATCTTGACTTAATTTTGAATGGCTTCTAGTAA 1522
 |||||||
 Db 19744 GCTTGATATATTTGTTGATTAATTAAGATCTTGACTTAATTTTGAATGGCTTCTAGTAA 19803
 Qy 1523 AAGGAATGATATATTTCTTGAAGACATCGATTAATTTTATTTAGCTCTGATCTCA 1582
 |||||||
 Db 19804 AAGGAATGATATATTTCTTGAAGACATCGATTAATTTTATTTAGCTCTGATCTCA 19863
 Qy 1583 ATGTAAATAATGAGAAATGCGCAAAATGTATGATGATTAAGTACGTAAAGAGCT 1642
 |||||||
 Db 19864 ATGTAAATAATGAGAAATGCGCAAAATGTATGATGATTAAGTACGTAAAGAGCT 19923
 Qy 1643 GATTGGTGCATCCAGGCTTTTGTCTGTGATGATGATCTCCCTTAAGCAATTCGA 1702
 |||||||
 Db 19924 GATTGGTGCATCCAGGCTTTTGTCTGTGATGATGATCTCCCTTAAGCAATTCGA 19983
 Qy 1703 AACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAAAGTTTCCACTGTATTTGAA 1762
 |||||||
 Db 19984 AACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAAAGTTTCCACTGTATTTGAA 20043
 Qy 1763 TCAGAAATGCTTCAACTGMAAAACATATCCAAATATGAGAAATGTGTGGCTCAC 1822
 |||||||
 Db 20044 TCAGAAATGCTTCAACTGMAAAACATATCCAAATATGAGAAATGTGTGGCTCAC 20103
 Qy 1823 TACGTAGATCCAGAGGAGAGTCAAGTCTTTAGGTTGCTGTATCCAGTAATCGGGCC 1882
 |||||||
 Db 20104 TACGTAGATCCAGAGGAGAGTCAAGTCTTTAGGTTGCTGTATCCAGTAATCGGGCC 20163
 Qy 1883 TGTTTCCCGTGGTCTCTGGGCTGTCAAGTCTTCTTCATGTTGTTGATTTCTCT 1942
 |||||||
 Db 20164 TGTTTCCCGTGGTCTCTGGGCTGTCAAGTCTTCTTCATGTTGTTGATTTCTCT 20223
 Qy 1943 CAGGCTGTGACAGTCTTGATCTTATACCAACACACAGCAACATCCAGAAATTAAGT 2002
 |||||||
 Db 20224 CAGGCTGTGACAGTCTTGATCTTATACCAACACACAGCAACATCCAGAAATTAAGT 20283
 Qy 2003 TCT 2005
 |||
 Db 20284 TCT 20286

RESULT 9

PCT-US03-03482-3147
 : Sequence 3147, Application PC/TUS0303482
 : GENERAL INFORMATION:
 : APPLICANT: Mendrick, Donna
 : APPLICANT: Porter, Mark
 : APPLICANT: Johnson, Kory
 : APPLICANT: Higgs, Brandon
 : APPLICANT: Castle, Arthur
 : APPLICANT: Orr, Michael
 : APPLICANT: Elashoff, Michael
 : TITLE OF INVENTION: Primary Rat Hepatocyte Toxicity Modeling
 : FILE REFERENCE: 44921-5113-WO
 : CURRENT APPLICATION NUMBER: PCT/US03/03482
 : CURRENT FILING DATE: 2003-02-04
 : PRIOR APPLICATION NUMBER: 60/353,171
 : PRIOR FILING DATE: 2002-02-04
 : PRIOR APPLICATION NUMBER: 60/363,534
 : PRIOR FILING DATE: 2002-03-15
 : PRIOR APPLICATION NUMBER: 60/371,135
 : PRIOR FILING DATE: 2002-04-10
 : PRIOR APPLICATION NUMBER: 60/371,134
 : PRIOR FILING DATE: 2002-04-10
 : PRIOR APPLICATION NUMBER: 60/370,248
 : PRIOR FILING DATE: 2002-04-08
 : PRIOR APPLICATION NUMBER: 60/371,150
 : PRIOR FILING DATE: 2002-04-10
 : PRIOR APPLICATION NUMBER: 60/371,413
 : PRIOR FILING DATE: 2002-04-11
 : PRIOR APPLICATION NUMBER: 60/373,601
 : PRIOR FILING DATE: 2002-04-19
 : PRIOR APPLICATION NUMBER: 60/374,139

Fri Apr 4 11:29:17 2003

us-09-967-305-1.rtf

Page 11

```

? PRIOR FILING DATE: 2001-07-09
? PRIOR APPLICATION NUMBER: US 60/331,273
? PRIOR FILING DATE: 2001-11-13
? Remaining Prior Application data removed - See File Wrapper or PALM
? NUMBER OF SEQ ID NOS: 4295
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3146
? LENGTH: 1504
? TYPE: DNA
? ORGANISM: Rattus norvegicus
? FEATURE:
? OTHER INFORMATION: Genbank Accession No. NM_012816
? CCT-0503-03194-3149

```

[illegible]

Oy	912	TGCTGCAAAATCTTTGAGCGACACAGATAGCTGTGTGACATCTCGGTTCTGACATTTTGAGGAG	972
Oy	912		
Db	842	TGCTGCCAATCTTTGAGCGACAGATATGATGTGTGACCCAGTGTGACATCTGTAGGAG	901
Oy	972	GTTTGTTCATCATGATCACAACACAGAAAGCGGGCTGTTATCACAGTAGAGACAGAC	1031
Oy	972		
Db	902	GCCCTCCACACACACACACACAGAAAGAGGGGGCTCTTCATCATCTGATGAGGAGAGCT	961
Oy	1032	GTGAGCCCCCGCCCTGTGACCTCTGTCTTTAAACACCCAGCCATCCCTTCTTTCAAAAG	1091
Oy	1092	GATCTCTTCATAGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTCAAGCCGCA	1151
Oy	1092		
Db	1022	GACCCCTCTGTGGGAGACACACACTGTAGAGTGCTTTAAAGACTATGATCAATCAATCGA	1081
Oy	1152	GAGATTTATCACCATTAACTCGATGAATAAATCATTTGAGAAATATTAAGTAAGTAAGCTGTGTC	1211
Db	1082	GATATCTCATCAGCTGCATCTGATAGATATCATTTGAAATATTAAGTAAAGCAACCTC	1141
Oy	1212	TAACTTCAGAGCCGACGGCTCAAGTAAATTTGAATACATGCTTACAGCTGTAGAGTACA	1271
Db	1142	TGACT--CAGGTTCAACCTTCAMGTAACTGAAAGCTGTATCTGTACTGAGAGAGATG	1199
Oy	1272	CATACATGTATGATGAGAAACATGAGAGAACGATATTACAGTGTCTTACCACTTAAT	1351
Db	1200	CCGACACAGCTCCGATATGAAATGTGAATGAACATTAATGAAGTAATCCAAATATTCCA	1259
Oy	1332	CAAGAAAGAAATTTACAGACCTGTGATTTCTACAGTGAATTTGAATTTCAAAATATGTTATC	1391
Db	1260	TCAAGACACACAGAAAG--CTGTTATACAGAAATAATGACTGTCTTCACACAGCTCATC	1317
Oy	1392	---ATTAGGCGCTTTGATTATTAACCTTTGGGTACTTATCTAATTAATGATGATTAAT	1448
Db	1318	CGAGCCTCGATTGAGAGATATTTTGTGTGTGTACTGATTAATCTGTGGCAGTT--TT	1376
Oy	1449	CTGCTTCCTCAGTTTCTGATATATT	1474
Db	1377	CTGCTTCCTCAGCTTACTTGTTGAAGT	1402
RESULT 11			
US-10-152-319A-1546			
Application US/10152319A			
GENERAL INFORMATION:			
APPLICANT: Mendlick, Donna			
APPLICANT: Porter, Mark			
APPLICANT: Johnson, Kory			
APPLICANT: Higgs, Brandon			
APPLICANT: Castle, Arthur			
APPLICANT: Blashoff, Michael			
TITLE OF INVENTION: Molecular Targeting Toxicology Modeling			
FILE REFERENCE: 44921-5089-US			
CURRENT APPLICATION NUMBER: US/10/152,319A			
PRIORITY FILING DATE: 2002-05-22			
PRIORITY APPLICATION NUMBER: US 60/292,335			
PRIORITY FILING DATE: 2001-05-22			
PRIORITY APPLICATION NUMBER: US 60/298,925			
PRIORITY FILING DATE: 2001-06-13			
PRIORITY APPLICATION NUMBER: US 60/303,810			
PRIORITY FILING DATE: 2001-07-10			
PRIORITY APPLICATION NUMBER: US 60/303,807			
PRIORITY FILING DATE: 2001-07-10			
PRIORITY APPLICATION NUMBER: US 60/303,808			
PRIORITY FILING DATE: 2001-07-10			
PRIORITY APPLICATION NUMBER: US 60/315,047			
PRIORITY FILING DATE: 2001-08-28			
PRIORITY APPLICATION NUMBER: US 60/324,928			
PRIORITY FILING DATE: 2001-09-27			
PRIORITY APPLICATION NUMBER: US 60/330,867			

RESULT 11
US-10-152-319A-1546
Sequence 1546, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867

```
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1546
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012816
US-10-152-319A-1546

Query Match      41.4%; Score 830; DB 8; Length 1504;
Best Local Similarity 76.3%; Pred. No. 2e-195;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4;

QY 72 CTGACAGGAGATCTGGTGTGAGAGCTGCGGCGCTGGCCCGGCGCTTGTGTATG 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2 CTGGGTGGCGCTCAGAGGTTCTGGAGCTGGCAGGCTGGCCCGGCGCTTGTGCGGGATG 61

QY 132 GTGCTGGGTGACTCGGGGCGCTGTGTGTAGCGTGGACCGGCGGCTTCCGCTAGAC 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 ATCTGTGGCGAGCTTGGCGCGGAGGTGTGCTGTGACAGACTGGGCTTCCGTGAACAC 121

QY 192 GTGAGCCGCTTGGCGCGGAGCAGCGCTGCTAGTGTGACGTGAACAGCCGCGGGA 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 122 CCGAGTACCTGCGCCCGAGCAGCGCTGCTGGCGGTGGAGCTGAAGCGGTCTCCGGA 181

QY 252 GCCCGCGTGTGCGCGGCTGTGCAAGCGGTGATGCTGTGCTGTGAGCCCTTCCGCGC 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 182 GCCCGGTGTGTGCGCGGCTGTGCAAGCGGTGATGCTGTGCTGTGAGCCCTTCCGCTG 241

QY 312 GGTGTGATGAGAACTCCAGCTGGGCCAGAGATTCGACGGGGAATAATCCAAAGCTT 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 242 GGTGTGATGAGAACTCCAGCTGGGCCAGAGACTCTACGGCAGAGCAATCCAAAGCTC 301

QY 372 ATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAAGAACTTCTCCGGTTAGTGGCCAC 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 ATTTATGCCAGGCTGAGTGTGATTTGGCCAGTGGGAAATTTCTCCAAAGTGTGGCCAT 361

QY 432 GATATCAACTTTGGCTTTGTCAAGTGTCTCCTCAAAATTTGGCAGAGTGTGAGATG 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 362 GACATCAACTATGTGCTTTGTCAAGTGTCTCCTCAAAATTTGGCAGAGTGTGAGATG 421

QY 492 CCGTATGCCCGGCTGATATCTGGCTGACTTGTGCTGTGGGCTTATGTGACTG 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 422 CCGTATGCCCGGCTGATATCTGGCTGACTTGTGCTGTGGGCTTATGTGACTG 481

QY 552 GGCATTAATATGCTCTTTTGGACGCAACGCACTGGCAAGGTCAGGTCATTGATGCA 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 482 GGCATTTTGTGCTCTCTTCTTGAACGCGGCTGTGGCCTTATGGGAGGTCATTGATGCG 541

QY 612 AATATGTGTGAAGAACAGCAATTTTCTGTGGAATTTGCAAAATTCGAGT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 AACTATGTGTGAAGAACAGCAATTTTCTGTGGAATTTGCAAAATTCGAGT 601

QY 672 CTGTGGGAAGACCTTCAGAGCAGACATGTTGATGTTGAGGAGACCTTTTATAGACT 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 602 CTGTGGGACAGCTTCAGAGGCAAAACCTTTTATAGTGGCGGAGACCTTTTATAGACCC 661

QY 732 TACAGGACAGCAGATGGGGAATTCATGCTTTGGAGCAATAGAACCCCAATTTAGAG 791
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 662 TACAGGACCGAGATGGGGAATTCATGCTTTAGTGTGAATAGAACCCCAATTTAGACA 721

QY 792 CTGCTGATCAAGACTTTGACTTAAGTCTGATGAATTTCCCAATCAGAGTGCATGAT 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 722 CTGCTGCTTAAAGACTTTGACTTGTGAGGAACCTCCACAGCAGATGAGATGAA 781

QY 852 GATTGGCCAGAAATGAGAAAGATTTGAGATATTTTGGAAAGAGAGAGAGAGAG 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 782 GATTGGCCAGAAATGAGAAAGATTTGAGATATTTTGGAAAGAGACTTAAGAGAGAG 841
```

```
QY 912 TGTGTCAAAATCTTTGAGGCGACAGATGCTGTGTGACTCGGCTTGTGACTTTTGAGAG 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 842 TGTGTCCAGATCTTTGAGGCGACAGATGCTGTGTGAGTCCAGGCTGTGACTTTTGAGAG 901

QY 972 GTTGTTCATCATGATTCACACAGAAAGAGGCGCTGCTTTATCAGCAGTGTGAGAGCAG 1031
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 902 GCCCTCCAGCACAGACACACAGAAAGAGGCGCTTCTTCACTGATGATGAGAGCAGCAT 961

QY 1032 GTGAGCCCGGCGCTGACCTCTGCTGTTAACACCCAGCAGCCTCTTCTTCAAAAG 1091
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 962 GCATGCCCCCTCTGACACCCAGCAGTTCAGAAACCCCTGCTGTCTTCCCTGCGCAAAAG 1021

QY 1092 GATCCTTTCAATAGAGAAACACACTGAGAGATCTTGAAGATTTGGATTGAGCGCGGAA 1151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1022 GACCTTCTGTGGGAGAGACACAGTGTAGAGGTGCTTAAAGACTATGATGATGAGAGGAA 1081

QY 1152 GAGATTTATACGCTTACTGATTAATAATCTTGAAGTATTAAGTAAAGTATGCTC 1211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1082 GAGATTCATGCTGACACTGATGATGATTAATTAAGTAAAGTATTAAGTAAAGTATGCTC 1141

QY 1212 TAACCTCAGCGCCAGCGCTCAAGTGAATTTGAATTAAGTATTAAGTATTAAGTATTAAG 1271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1142 TGAAT--CAGGTTACACAGCTCAAGTGAATTTGAAGGCTGTATCTGTACTGAGAGAGATG 1199

QY 1272 CATACATTTGATGATGAGAAACATGAGGAGACAGTATTAAGTATTAAGTATTAAGTATTAAG 1331
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1200 CCGACACACTGCTCGCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1259

QY 1332 CAAGAAAGATTTACAGACTGATTTCTACAGTATGATGATGATGATGATGATGATGATGATGAT 1391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1260 TCAAGACACAGAAAG--CTGATTTACAGAGAAATGATGATGATGATGATGATGATGATGATGAT 1317

QY 1392 --ATTAAGGCTTTGATTTAATAACCTTTGGTACTTATCTAATTAATGATGATGAT 1448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1318 CGAGCTCTGATTTGAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1376

QY 1449 CTGCTTCCAGCTTTGATGATTAAT 1474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1377 CTGCTTCCAGCTTTGATGATTAAT 1402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-10-301-856-852
; Sequence 852, Application US/10301856
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Portier, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Nephrotoxicology Modeling
; FILE REFERENCE: 44921-5089-01
; CURRENT APPLICATION NUMBER: US/10/301,856
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
```



```

: PRIOR FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: US 60/330,867
: PRIOR FILING DATE: 2001-11-01
: Remaining Prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 1261
: SOFTWARE: Patentl Ver. 2.1
: SEQ ID NO 852
: LENGTH: 1504
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. NM_012816
US-10-301-856-852

```

```

Query Match 41.4%: Score 830: DB 8: Length 1504:
Best Local Similarity 76.3%: Pred. No. 2e-195:
Matches 1073: Conservative 0: Mismatches 325: Indels 8: Gaps 4:

QY 72 CTCGAGGCAATCTCGTGTGGACCTTCGCGCCCTGCGCCCGCGCTTCGTGCTATG 131
DB 2 CTCGAGGCAATCTCGTGTGGACCTTCGCGCCCTGCGCCCGCGCTTCGTGCTATG 61
QY 132 GTCCTGGCTGACTTGGGGCGCGTGTGACGCGTGAGCCGCGCTCCCGCTACGAC 191
DB 62 ATCTGGGCGACTTGGGGCGCGAGGTGTGTCTGTGTGACAGACTGGCTCCGTGACCC 121
QY 192 GTGAGCGGCTTGGGGCGCGGCGCTGCTAGTGTGTGAGCTGAGACCGCGGGGA 251
DB 122 CCCAGTACACTGCGCCGAGGCGAGCGCTGCGCTGCGCTGAGACGCGTCCGGGA 181
QY 252 GCGCGCGTCTGCGCGCTGCTGTGCAAGCGGTGCGATGTGTGAGACCGCTCCGCGC 311
DB 182 GCGCGCGTCTGCGCGCGATGTGTGCGACGCGCGAGCTGTGTCTGTGAGACCGCT 241
QY 312 GGTGTATGGAAGAACTCCAGTGGGCGCAGAGATTTCTGACGGGAAATTCAGAGCTT 371
DB 242 GGTGTATGGAAGAACTCCAGTGGGCGCAGAGACTCTAGCGGAGAGACATCCAAAGCTC 301
QY 372 ATTTAGCCAGCGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCGCGGTGTAGCGGCAC 431
DB 302 ATCTAGCCAGCGCTGAGTGGATTTGGCCAGTCCGGAATTTCTCCAAAGTACGTGGCAT 361
QY 432 GATATCAACTATTTGGCTTTGTCAAGTGTCTCAAAAATTTGGCAGAGTGTGAGAT 491
DB 362 GACATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAAC 421
QY 492 CCGTATGCGCGCTGAATCTCTGTGACTGCTGTGTGTGTGTGTGTGTGTGTGTGTG 551
DB 422 CCGTATGCGCGCTGAATCTCTGTGACTGCTGTGTGTGTGTGTGTGTGTGTGTGTG 481
QY 552 GGCATTATATGCTCTTTTGTACCGCAGCAGCAGTGGGCTGAGGCTTATGTGATGCA 611
DB 482 GGCATTATATGCTCTTTTGTACCGCAGCAGCAGTGGGCTGAGGCTTATGTGATGCG 541
QY 612 AATATGTTGAAGAAAGCATATTTTAACTTTTCTGTGGAAGAAATCAGAAATCGAGT 671
DB 542 AACATGTTGAAGAAAGCATATTTTAACTTTTCTGTGGAAGAAATCAGGCAATGGGT 601
QY 672 CTGTGGAAGCACTCGAGGAGCAGACATGTGTGATGTGGAGCACTTCTATACAGCT 731
DB 602 CTGTGGAAGCACTCGAGGAGCAGACATGTGTGATGTGGAGCACTTCTATACAGC 661
QY 732 TAAGAGACAGCAGATGGGGAATTTATGCTGTGTGAGCAATAGAACCCAGTTCTACAG 791
DB 662 TAAGAGACAGCAGATGGGGAATTTATGCTGTGTGAGCAATAGAACCCAGTTCTACACA 721
QY 792 CTGCTATCAAGAGACTTGAAGTGTGATGAAGTTCCTCCATTCAGATGAGATGAT 851
DB 722 CTGCTATCAAGAGACTTGAAGTGTGATGAAGTTCCTCCATTCAGATGAGATGAGAA 781
QY 852 GATTGGCCAGAAATGAAGAAAGTTTGAGATGTATTTTGCAAGAAAGCAAGAGAG 911
DB 782 GATTGGCCAGAAATGAAGAAAGTTTGAGATGTATGTGTTTGCAAGAAAGCAAGAGAG 841

```

```

QY 912 TGGTGTCAAAATCTTTGAGCGCAGATGCTGTGTGATCCCGTTCGTGACTTTGAGAG 971
DB 842 TGGTGTCAAAATCTTTGAGCGCAGATGCTGTGTGATCCCGTTCGTGACTTTGAGAG 901
QY 972 GTTGTTCATGATGATCAACAGAGAGGAGGCTGTTTATACCAAGAGAGAGAGAG 1031
DB 902 GCCCTCCACACACAGCAGACAGAGAGAGGAGGCTCTTCATCATGATGAGAGAGAG 961
QY 1032 GTGAGCGCGCGCGCTGAGCAGCTGTGTAAACCCGAGCATCCCTTTTGAAGG 1091
DB 962 GCATGCGCGCGCTGAGCAGCAGCAGCTTTCCAGAGACCCCTGCTTCTTCCAGAA 1021
QY 1092 GATCTTTTATGAGAGACACACTGAGAGATGCTTGAAGATTTGGATTTACCGCGAA 1151
DB 1022 GACCTCTTGTGTGAGAGACACACTGAGAGATGCTTGAAGATTTGAAGATTTGAGAG 1081
QY 1152 GAGATTTATCAGCTTAACTCAATTAATCATTTGAAGATTAAGTAAAGCTATGCTC 1211
DB 1082 GAGATTTATCAGCTTAACTCAATTAATCATTTGAAGATTAAGTAAAGCTATGAG 1141
QY 1212 TAACTTCAAGCGCGCTCAAGTGAATTTGAATGATGATTTACAGTGTAGAGTACA 1271
DB 1142 TGACT--CAGTTTCAAGCTCAAGTGAATTTGAAGTGTATGATGATGAGAGATG 1199
QY 1272 CATACATTTGATGATGAGAGAGAGAGAGAGATTTACAGTGTCTTACACTTAAT 1331
DB 1200 CCCACACAGCTCGATGAGAAATGAGATGAGATGAGATGAGATGAGATGAGATG 1259
QY 1332 CAAGAAAGATTTACAGCTGATTTACAGTGTGATTTGAATTTGAATTTGATTTATC 1391
DB 1260 TCAAGACACAGAGAAAG--CTGATTTACAGAGAAATGATGATGATGATGATGATG 1317
QY 1392 ---ATTAGGCGCTTTGATTTAAACTTTGGGTACTTAACTTAAATTAAGTGTGAT 1448
DB 1318 CGAGCGCTGTGAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1376
QY 1449 CTGCTTCCAGTTTGTGTGATTTAT 1474
DB 1377 CTGCTTCCAGTTTGTGTGATTTAT 1402

RESULT 13
US-10-338-044-1802
: Sequence 1802, Application Us/10338044
: GENERAL INFORMATION:
: APPLICANT: MENDRICK, Donna
: APPLICANT: PORTER, Mark
: APPLICANT: JOHNSON, Kory
: APPLICANT: HIGGS, Brandon
: APPLICANT: CASTLE, Arthur
: APPLICANT: ELASHOFF, Michael
: TITLE OF INVENTION: Molecular Cardiototoxicology Modeling
: FILE REFERENCE: 44921-5090-01-US
: CURRENT APPLICATION NUMBER: US/10/338,044
: PRIOR FILING DATE: 2003-01-27
: PRIOR APPLICATION NUMBER: US 60/303,819
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: US 60/305,623
: PRIOR FILING DATE: 2001-07-17
: PRIOR APPLICATION NUMBER: US 60/369,351
: PRIOR FILING DATE: 2002-04-03
: PRIOR APPLICATION NUMBER: US 60/377,611
: PRIOR FILING DATE: 2002-05-06
: NUMBER OF SEQ ID NOS: 2696
: SOFTWARE: Patentl Ver. 2.1
: SEQ ID NO 1802
: LENGTH: 1504
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. NM_012816
US-10-338-044-1802

```


D	182	GGCGCGGTTGGTGGCGGATGTGGGACGGCGGGAGCTGTGGTGGAGCCCTTCCTTCC	241
O	312	GGTGTATGGAAACCTCAGCTGGGGCCAGAGATTCTGCAGCGGGAAATCCAAAGCTT	371
D	242	GGGTGATGGAAACCTCAGCTGGGGCCAGAGACTCTACGGCAGGACATTCMAAGTTC	301
O	372	ATTATGCGAGGCTAGTGGATTGGGCGAGTCAGAGACCTTCGCGGTTAGTGGGCCAC	431
D	302	ATCTATGCCAGGCTAGTGGATTGGGCGAGTCGGGAATTTCTCCAAAGTACGTGGCCAT	361
O	432	GATATCACTATTGGCTTTGTACAGGTGTCTCAAAAATTGGCCACAGCTGGTAGAT	491
D	362	GACATCACTATGTGGCTTTGTACAGGTGTCTCTCAAAATTGGCCAGAGCGTTGAAAC	421
O	492	CGGTATGCCCGCTGAATCTCCGCTGACTTTCGTGGTGGCTTATGTGTGACTGT	551
D	422	CCATACCTCCCTAACCTCTGCGCGAATTTGGGGGGGGGCTCATGTGCACATTTG	481
O	552	GGCATTTAATGGCTCTTTTGGACCGCACGCACTGGCAAGGTCAGTCAATTATGCA	611
D	482	GGGATTTCTGGCTCTCTTGGAAACGACAGCGGTCTGGCTTAGGGGCAAGTATGTGG	541
O	612	AATATGTGGAAAGAACAGCATATTTAAGTCTTTCTGTGGAAAACTCAGAAATGAGT	671
D	542	AACATGTGGAAAGAACAGCATATTTAAGTCTTTCTGTGGAAAACTCAGGCGCATGGGT	601
O	672	CTGTGGGAAGCACCTTCGAGGACAGAACATGTGTGATGTGTGACACCTTTCTATACAGT	731
D	602	CTGTGGGCGACACCTTCGAGGGCAAAACCTGTATAGATGGCGGGGCACTTTCTACAAAC	661
O	732	TACAGACAGCAGATGGGGAAATTCATGGCTGTGGAGCAATAGAAACCCAGTTCTACAG	791
D	662	TACAAACCGCAGATGGGGAAATTCATAGGCTGTAGGCAATAGAAACCCAGTTCTACACA	721
O	792	CTGCTATCAAAAGACTTGGACTTGAAGTGTGATGAATCTCCCATCCAGATGAGCATGAT	851
D	722	CTGCTCTTAAAGACTTGGACTTGAAGTGTGATGAATCTCCCATCCAGATGAGCATAGAA	781
O	852	GATTGGCCGAATAGAAAGAAAGTTTGGAGATTTTGGCAAGAAAGACGAGAGGAGAG	911
D	782	GATTGGCCGAATAGAAAGAAATTTTGCAGATGTCTTTCAGAAAGACATAGAGCAGAG	841
O	912	TGTGTCAAATCTTGGAGCGACAGAGTCCGTGTGTGACTCCGGTCTTGACTTTTGAGGAG	971
D	842	TGTGTCAAATCTTGGAGCGAGATGTGTGTGTGACCCAGTGTCTTGACTTTTGAGGAG	901
O	972	GTTGTTCATCATGATCACACAAAGGAACGGGGCTCGTTATCACCAAGTAGAGACAGAC	1031
D	902	GCCCTCACACACACAAAGGAAGAGGGGGCTCCTTCATCATGATGAGAGAGCAT	961
O	1032	GTGAGCCCCCGGCTGCACCTCTGTCTGTATTAACACCCCAAGCCATCCCTTCTTCAAAAG	1091
D	962	GCAATGCCCGGCTGCACCCAGCTTTCACAAACCCCGCTGTTCTCTTCTGCCAAAG	1021
O	1092	GATCTCTTATAGGAACACAGTGAAGATACTTGAAGAAATTTGGATTACACCGCGAA	1151
D	1022	GACCTCTTGTGGGAGACACACTGTGAGGTCTTAAAGACTATGATTTCACTCAGGAA	1081
O	1152	GACATTTATCACCTTAACCTCAGATTAATTAATCATTTGAAAGTAATAGTAAGTAAGTACTCTC	1211
D	1082	GAACTCACTACCTCTCACTCGATAGAAATCATTTGAAAGTAATTAAGTAAAGCCACCTC	1141
O	1212	TAACTTCAGGCGCCAGGCTCAAGTGAATTTGAATACCTGACTTTACAGTGAAGTAACTA	1271
D	1142	TGACT--CAGGTTTCACACTCAAGTGAATCTGAAGCTGTATCTGTACTGGAAGGAAG	1191
O	1272	CATACATTTATGATGATGGAACATGGAGAACAGTATTAACAGTGTCTTACACCTTAAT	1331
D	1200	CCCAACACGTCCGATGGAATATGAAATGAACAGATTAAGAAATTCACAAATATTTCCA	1251
O	1332	CAGAAGAAATTTACAGACTGTGAATCTTCAAGTATGATTTGAATTTCAAAATGTTATTC	1391

```

Db 1260 TCAGACACAGCAAGAAAG--CTGATTACAGAGAAATACAGTCTCTCACACTGCTATC 1317
Oy 1392 ---ATTAGAGCCCTTTTGAATTATAAACCTTTGGCTACTTATACATAAATTTGGTATATT 1448
Db 1318 CGAGCCTCGATTGAGGAGTATTTTGTGTGTGATCGATATTAACCTTGTGCGAGTTT 1376
Oy 1449 CTCGCTTCAGCTTGGCTTGTGATATT 1474
Db 1377 CTCGCTTCAGCTTACTTGTGTGAAGT 1402

RESULT 15
US-60-436-643-3149
; Sequence 3149, Application US/60436643
; GENERAL INFORMATION:
; APPLICANT: Mendlick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
; FILE REFERENCE: 44921-5038-P15
; CURRENT APPLICATION NUMBER: US/60/436, 643
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4295
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3149
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012816
US-60-436-643-3149

Query Match 11.4%; Score 830; DB 9; Length 1504;
Query Similarity 76.3%; Pctd. No. 2e-195;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4

Oy 72 CTCGACGAGCATCTGGCTGTCGAGACCTGTCGCGCTCGCCCGGCGCCCTTCTGTGCTATG 131
Db 2 CTCGCTGTGGGTGAGGCTTCTGGAGCTCGGAGGCTCGGCCACGAGGCGCGCTTCTGCGGAGT 61
Oy 132 GTCCTGCTGACTTGTGGGCGCGCTGTGTGACCGGTGACCGCGCCGCTCCCGCTACGAC 191
Db 62 ATCTCTGCGCGAATTCCTGGCGCGGAGGTGTGCTCGTGACACAGACTGTGGCTCTGTAAACCA 121
Oy 192 GTGAGCCGCTGTGGGCGGAGCAAGCGCTTGCTAGTGTGTGACCTGTAAGCAGCAGCGCGGAGA 251
Db 122 CCCAGTCACTGTGGCGCGAGGCAAGCCCTCTGCTGGCGGCTGAGACCTGAAGCGGTCTCGGGA 181
Oy 252 GCCGCGCTGTGTCGCGGCTCTGTGTCAAGCGTGTGATGTGCTGTGAGAGCCCTTCCGCGC 311

```

Db 182 GCCCGGGTGTGCGCCCACTGCGCACGGCGGACGCTGTGGGAGCCCTTCCGTGCG 241
 Qy 312 GGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCGTGACGGGGAAATCCAGGCTT 371
 Db 242 GGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCGTGACGGGGAAATCCAGGCTT 301
 Qy 372 ATTTATCCAGGCTGAGTGGATTTGGCCAGTCCAGAAAGCTTCTGCGGTAGCTGGCCAC 431
 Db 302 ATCTATGCCAGGCTGAGTGGATTTGGCCAGTCCAGAAAGCTTCTGCGGTAGCTGGCCAT 361
 Qy 432 GATATCACTATTTGGCTTTGTCTGAGTGTCTCTCAAAATTTGGCAGAAAGTGGTGAAT 491
 Db 362 GACATCAACTATGTGCTTGTCTGAGTGTCTCTCAAAAGTGGCAGAGGGGAGAAC 421
 Qy 492 CCGATATCCCGCTGATTCCTGCTGACTTTGCTGAGTGGCTTATGTGCACTG 551
 Db 422 CCATACCTCTCCCTGAACTCTGCGGACTTTGTGGCGGTGCTCATGTGCACTTGC 481
 Qy 552 GGCATTTAAATGGCTCTTTTGTGACGCAACGCACTGGCAAGGTCAGGTGATGCA 611
 Db 482 GGCATTTTGTGCTGCTCTCTGAAACGCAAGGCTGCGCTAGGGCAGGTGATGCG 541
 Qy 612 AATTGTGAGAGAAACAGCATATTTAAGTCTTTCTGTGAAAACCTCAGAAATCGAGT 671
 Db 542 AACATGTTGAGAGAAACAGCATATTTAAGTCTTTCTGTGAAAACCTCAGAGCCATGGT 601
 Qy 672 CTGTGGAAACACCTTCAGAGACAGAAACATGTGGATGGTGAGCACTTCTATAGCACT 731
 Db 602 CTGTGGGACACAGCTTCAGAGGCAAAACCTGTAGATGGCGGGCACTTTCTACACAAC 661
 Qy 732 TACAGGACAGCATGGGGAAATTCAGTGTGGTGGCAATAGAACCCAGTCTACGAG 791
 Db 662 TACAAAGACCCGAGTGGGAGTTCATGTGAGTGAATAGAACCCAGTCTACACA 721
 Qy 792 CTGCTGATCAAGGACTTGGACTTAAGCTGATGAACCTCCCATTCAGATGAGCATGAT 851
 Db 722 CTGCTGCTTAAAGACTTGGACTTGAATCTGAGGAACTCCCGACGAGATGAGCATGAA 781
 Qy 852 GATTGGCCAGAAATGAAAGAAAGTTCGAGATGATTTGCAAAAGAGACGAAAGGCGAG 911
 Db 782 GATTGGCCAGAAATGAAAGAAAGTTCGAGATGATTTGCAAAAGAGACGAAAGGCGAG 841
 Qy 912 TGGTGTCAATCTTTGACGCGACAGATGCTGTGACTCGGTTCTGACTTTGAGGAG 971
 Db 842 TGGTGTCAATCTTTGACGCGACAGATGCTGTGACTCGGTTCTGACTTTGAGGAG 901
 Qy 972 GTTGTGATGATGATCAACAAGAGAGGAGGCTGTTTATCACCAGTGAAGAGCAGGAC 1031
 Db 902 GCCCTCCACCAACGACGACGAGAAAGGAGGCTCTTCTCATCTGATGAGGAGCAGCAT 961
 Qy 1032 GTGAGCCCGCCGCTGACCTGTGTTAAACCCGACGACCTCTTTTCAAAAGG 1091
 Db 962 GCATGCCCGCCGCTGACCCGACTTTCAGAAACCCGCTGTTCTTCCCTGCCAAAGG 1021
 Qy 1092 GATCTTTCAATAGAGAAACACAGAGATGATTTGAAGAAATTTGATTCAGCGCGAA 1151
 Db 1022 GACCTTTCTGTGGGAGACACAGTGAAGTGTCTTAAAGCTATGATTCAGTCAAGAA 1081
 Qy 1152 GAGATTTATCAGCTTAACTCAGATTAATCATTTGAAAGTAAATAGGTAAGGTAAGCTAGCTC 1211
 Db 1082 GAGATTCATCAGCTGCACTGAGTGAATCATTTGAAAGTAAATAGCTAAAGCCACACCTC 1141
 Qy 1212 TAACTTCAGGCGCCAGGCTCAAGTGAATTTGAATTAAGTCAATTTACAGTGAAGTAA 1271
 Db 1142 TGAATTCAGGCTCAAGTGAATTTGAATTAAGTCAATTTACAGTGAAGTAA 1199
 Qy 1272 CATTAATTTATGATGAGAAACATGAGAGACGATTTACAGTGTCTTACACTTAAT 1331
 Db 1200 CCAACCTGCTGCTGAGAAATGTAATGAATGAATGAATGAATGAATGAATGAATGAAT 1259
 Qy 1332 CAGAAAGAAATTAACAGTCTGATTTACAGTGAATGAATGAATGAATGAATGAATGAAT 1391

Db 1260 TCAAGACACAAGAAAGA--CTGATTAACAGAGAAATGACTGTGCTCTCACACTGCTCATC 1317
 Qy 1392 ---ATTAGGCTTTTGAATTAATAAACTTTGGTACTTATTAATTAATTAATTAATTAAT 1448
 Db 1318 CGAGCCCTGATTAAGAGATATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1376
 Qy 1449 CTGCTTCCAGTTTGTGTTGATTAATTT 1474
 Db 1377 CTGCTTCCAGTTTGTGTTGATTAATTT 1402

Search completed: April 2, 2003, 02:48:31
 Job time : 718.574 secs


```

OY 241 AGCCGGGGAGCCGCCGCTGCTGTGCAAGCGGCTCGATGCTGCTGGAGC 300
    |||||
Db 241 AGCCGGGGAGCCGCCGCTGCTGTGCAAGCGGCTCGATGCTGCTGGAGC 300
OY 301 CCTTCGGCGGGTGCATGAGAACTCCAGTGGGCCGAGATTCGACAGGGAAA 360
    |||||
Db 301 CCTTCGGCGGGTGCATGAGAACTCCAGTGGGCCGAGATTCGACAGGGAAA 360
OY 361 ATCCAAGCTTATTTATGCGAGGCTAGTGGATTTGGCCAGTCAGAACTTCGCGGT 420
    |||||
Db 361 ATCCAAGCTTATTTATGCGAGGCTAGTGGATTTGGCCAGTCAGAACTTCGCGGT 420
OY 421 TACCTGGCCACGATATCACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAA 480
    |||||
Db 421 TACCTGGCCACGATATCACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAA 480
OY 481 GTGTGAGAAATCCGTATGCCCCGCTGAATCTCTGCTGCTTTGCTGGTGGGCGCTTA 540
    |||||
Db 481 GTGTGAGAAATCCGTATGCCCCGCTGAATCTCTGCTGCTTTGCTGGTGGGCGCTTA 540
OY 541 TGTGTGCACTGGGCAATTAATGCTCTTTTGTACCGCACAGCAGCTGCGAAGGTCAGG 600
    |||||
Db 541 TGTGTGCACTGGGCAATTAATGCTCTTTTGTACCGCACAGCAGCTGCGAAGGTCAGG 600
OY 601 TCATGATGCAAAATATGTTGGAAGAAAGACATATTTAAAGTCTTTCTGTGGAAGAACTC 660
    |||||
Db 601 TCATGATGCAAAATATGTTGGAAGAAAGACATATTTAAAGTCTTTCTGTGGAAGAACTC 660
OY 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGAGAGAAACATGTTGGATGGGAGCACTT 720
    |||||
Db 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGAGAGAAACATGTTGGATGGGAGCACTT 720
OY 721 TCTATACGACTTACAGAGACAGATGAGGGAATTCATGCTGTGGAGCAATGGAACCC 780
    |||||
Db 721 TCTATACGACTTACAGAGACAGATGAGGGAATTCATGCTGTGGAGCAATGGAACCC 780
OY 781 AGTTTACGAGCTGTGATCAAAAGAACTTGGACTAAAGTGTATGAACCTTCCCAATCAGA 840
    |||||
Db 781 AGTTTACGAGCTGTGATCAAAAGAACTTGGACTAAAGTGTATGAACCTTCCCAATCAGA 840
OY 841 TGAAGCATGATGATGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAGAGAGA 900
    |||||
Db 841 TGAAGCATGATGATGGCCAGAAATGAAGAAAGTTTGCAGATGATTTGCAAGAGAGA 900
OY 901 CGAAGCAGAGTGTGTCAAATCTTTGACGCGACAGATGCTGTGACTGCCGTTCTGA 960
    |||||
Db 901 CGAAGCAGAGTGTGTCAAATCTTTGACGCGACAGATGCTGTGACTGCCGTTCTGA 960
OY 961 CTTTGTAGGAGGTTGTTTCATCATGATCACAACAAGAACGGGCTGTATATCACAAGTG 1020
    |||||
Db 961 CTTTGTAGGAGGTTGTTTCATCATGATCACAACAAGAACGGGCTGTATATCACAAGTG 1020
OY 1021 AGGAGGAGCAGTGTGAGCCCCGCGCTGACCTGTGCTGTAAACACCCGACCATCCTT 1080
    |||||
Db 1021 AGGAGGAGCAGTGTGAGCCCCGCGCTGACCTGTGCTGTAAACACCCGACCATCCTT 1080
OY 1081 CTTTCAAAAGGATCTTTTCATGAGAAACACACTGAGGAGATCTGGAAGAAATTTGGAT 1140
    |||||
Db 1081 CTTTCAAAAGGATCTTTTCATGAGAAACACACTGAGGAGATCTGGAAGAAATTTGGAT 1140
OY 1141 TCAGCGCGGAGAGATTTATCAGCTTAACCTAGATTAATCATTGAAAGTAATAGGTAA 1200
    |||||
Db 1141 TCAGCGCGGAGAGATTTATCAGCTTAACCTAGATTAATCATTGAAAGTAATAGGTAA 1200
OY 1201 AACCTAGTCTTAACCTTCAAGCGCCACGGCTCAAGTGAATTTAAATACGATTTACAGT 1260
    |||||
Db 1201 AACCTAGTCTTAACCTTCAAGCGCCACGGCTCAAGTGAATTTAAATACGATTTACAGT 1260
OY 1261 GTAGAGTAACATATGATGATGAGAAACATGAGGAACAGATTTATACAGTGTCTT 1320
    |||||
Db 1261 GTAGAGTAACATATGATGATGAGAAACATGAGGAACAGATTTATACAGTGTCTT 1320
OY 1321 ACCACTCTAATCAAGAAAGAAATTAACAGACTGTGATTTCTACAGTATGATTTGAATCTTAA 1380
    |||||

```

```

Db 1321 ACCACTCTAATCAAGAAAGAAATTAACAGACTGTGATTTCTACAGTATGATTAATCTTAA 1380
    |||||
OY 1381 AAATGTTATCATTTAGGCGCTTTGATTTTAAACCTTGGGTACTATATCTAAATATG 1440
    |||||
Db 1381 AAATGTTATCATTTAGGCGCTTTGATTTTAAACCTTGGGTACTATATCTAAATATG 1440
OY 1441 TACTTATTCGCCCTTCAGTTGCTTGATATATTTGTTGATATTAAGATTCCTGACTAT 1500
    |||||
Db 1441 TACTTATTCGCCCTTCAGTTGCTTGATATATTTGTTGATATTAAGATTCCTGACTAT 1500
OY 1501 ATTTTGAATGGTCTTAGTGAAGAAAGAAATGATATATTTCTTGAAGCATCGATATCAT 1560
    |||||
Db 1501 ATTTTGAATGGTCTTAGTGAAGAAAGAAATGATATATTTCTTGAAGCATCGATATCAT 1560
OY 1561 TATTTACACTCTGATTTTCAATGATGAGAAATGAGAAATGCGCAAAATTTGATGTTGA 1620
    |||||
Db 1561 TATTTACACTCTGATTTTCAATGATGAGAAATGAGAAATGCGCAAAATTTGATGTTGA 1620
OY 1621 TAAAGTCAAGTGAAGAACAGAGTATGTTGATTCATCCAGGCGCTTTGTCTGTTCTATG 1680
    |||||
Db 1621 TAAAGTCAAGTGAAGAACAGAGTATGTTGATTCATCCAGGCGCTTTGTCTGTTCTATG 1680
OY 1681 ATCTCCCTCTAAGCACAATTCGAACTTTAGCAACAGTATACACTTTGTAATTTGCAAA 1740
    |||||
Db 1681 ATCTCCCTCTAAGCACAATTCGAACTTTAGCAACAGTATACACTTTGTAATTTGCAAA 1740
OY 1741 GAAAGTTTCACTGTATGATGATCAGATGCGCTTCAAGTGAAGAAAGAAATATATCAAAATA 1800
    |||||
Db 1741 GAAAGTTTCACTGTATGATGATCAGATGCGCTTCAAGTGAAGAAAGAAATATATCAAAATA 1800
OY 1801 ATGAGGAAATGTTGGCTCTACTAGCTAGAGTCCAGAGGAGACAGTCAATTTAGGGTTGC 1860
    |||||
Db 1801 ATGAGGAAATGTTGGCTCTACTAGCTAGAGTCCAGAGGAGACAGTCAATTTAGGGTTGC 1860
OY 1861 CTGTATCCAGTAACCTGGGGGCTGTTCCCGGTGGGTCTCTGGGCTGTAGCTTCTCTT 1920
    |||||
Db 1861 CTGTATCCAGTAACCTGGGGGCTGTTCCCGGTGGGTCTCTGGGCTGTAGCTTCTCTT 1920
OY 1921 CTCATGTGTTGATTTCTCTCAGGCTGTGTAGCAAGTCTGATCTTATACCAACACA 1980
    |||||
Db 1921 CTCATGTGTTGATTTCTCTCAGGCTGTGTAGCAAGTCTGATCTTATACCAACACA 1980
OY 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
    |||||
Db 1981 CAGCAACATCCAGAAATTAAGTTCT 2005

RESULT 2
US-09-967-305-10
; Sequence 10, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
; FILE REFERENCE: REFRACTORY AND METASTATIC PROSTATE CANCERS
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1211)
US-09-967-305-10

```


APPLICANT: Richardson, Jennifer
APPLICANT: Monahan, John
TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
TITLE OF INVENTION: REPRODUCTORY AND METASTATIC PROSTATE CANCERS
FILE REFERENCE: 07334-312001
CURRENT APPLICATION NUMBER: US/09/967, 305
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/236, 238
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2069
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)...(1235)
US-09-967-305-4

Query Match 99.9%; Score 2003.4; DB 10; Length 2069;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGCAGGCTGCTGGGCTGAAGGCTGCTCAGTTTCCTTCACGGGGGCACTGGGAA 60
DB 25 TTGCAGGCTGCTGGGCTGAAGGCTGCTCAGTTTCCTTCACGGGGGCACTGGGAA 84
QY 61 GGCCGATGAGCTGAGGAGGATCGGCTGAGAGCTGTCGGGCGGCGGCGGCGCT 120
DB 85 GGCCGATGAGCTGAGGAGGATCGGCTGAGAGCTGTCGGGCGGCGGCGGCGCT 144
QY 121 TCTGTGTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 145 TCTGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
QY 181 CCCGCTACGACGTGAGCGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCT 240
DB 205 CCCGCTACGACGTGAGCGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCT 264
QY 241 AGCCGCGGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 265 AGCCGCGGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
QY 301 CCTTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 325 CCTTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
QY 361 ATCCAAAGGCTTATTTATGAGCGAGGCTGATTTGGCCAGTCAAGGCTTCTGCGG 420
DB 385 ATCCAAAGGCTTATTTATGAGCGAGGCTGATTTGGCCAGTCAAGGCTTCTGCGG 444
QY 421 TAGCTGCGCAGATATCAATATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 445 TAGCTGCGCAGATATCAATATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 504
QY 481 GTGGTGAAGATCCGATATGCCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCT 540
DB 505 GTGGTGAAGATCCGATATGCCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCT 564
QY 541 TGTGTGACGAGGATATATGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 565 TGTGTGACGAGGATATATGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 601 TCATTTGATGAATATGATGATGAGGAGACAGCATATTTAAATTTCTTTCTGTAATCTC 660
DB 625 TCATTTGATGAATATGATGATGAGGAGACAGCATATTTAAATTTCTTTCTGTAATCTC 684
QY 661 AGAAATGAGCTGTGTGGAAGACCTTCGAGAGACAGAAATGTTGATGTGTGAGACCTT 720
DB 685 AGAAATGAGCTGTGTGGAAGACCTTCGAGAGACAGAAATGTTGATGTGTGAGACCTT 744
QY 721 TCATATGAGCTTACAGACAGCATATGAGGATTTGATGCTGTTGGAGCAATAGAACCC 780

DB 745 TCATATGAGCTTACAGACAGCATATGAGGATTTGATGCTGTTGGAGCAATAGAACCC 804
QY 781 AGTTTACGAGCTGCTGATCAAGGAGCTTGGATTAAGTGTGTAAGTCTTCCCATCAGA 840
DB 805 AGTTTACGAGCTGCTGATCAAGGAGCTTGGATTAAGTGTGTAAGTCTTCCCATCAGA 864
QY 841 TGAGCATGATGATTTGGCCAGAAATGAGAAAGTGTGAGATGATTTGGCAAGAGA 900
DB 865 TGAGCATGATGATTTGGCCAGAAATGAGAAAGTGTGAGATGATTTGGCAAGAGA 924
QY 901 CGAAGCAGAGTGTGCTCAATCTTTGACGCGACACATGCTGTGATCTCCGCTTCTGA 960
DB 925 CGAAGCAGAGTGTGCTCAATCTTTGACGCGACACATGCTGTGATCTCCGCTTCTGA 984
QY 961 CTTTGGAGGATTTGATCATGATCACAACAAGGAGGAGGCTGCTTATCAGCAGTG 1020
DB 985 CTTTGGAGGATTTGATCATGATCACAACAAGGAGGAGGCTGCTTATCAGCAGTG 1044
QY 1021 AGGAGCAGAGCTGAGCGCCCGCTGACCTGCTGCTTAAACACCCAGCCATCCCTT 1080
DB 1045 AGGAGCAGAGCTGAGCGCCCGCTGACCTGCTGCTTAAACACCCAGCCATCCCTT 1104
QY 1081 CTTTCAAAAGGATCCTTTGATAGGAGACACATGAGGAGATGATTTGAATTTGGAT 1140
DB 1105 CTTTCAAAAGGATCCTTTGATAGGAGACACATGAGGAGATGATTTGAATTTGGAT 1164
QY 1141 TCAGCCGCGAAGATTTATCACTTAACATCAATTAATCAATTAATTAATTAATTA 1200
DB 1165 TCAGCCGCGAAGATTTATCACTTAACATCAATTAATCAATTAATTAATTAATTA 1224
QY 1201 AAGCTAGCTCTTAACCTTCCAGGCGGCTCAAGTGAATTTAATTCGATTTACAGT 1260
DB 1225 AAGCTAGCTCTTAACCTTCCAGGCGGCTCAAGTGAATTTAATTCGATTTACAGT 1284
QY 1261 GTAGAGTAAACATTAATGATGATGAGAAATGAGAAATGAGAAATGAGAAATGAG 1320
DB 1285 GTAGAGTAAACATTAATGATGATGAGAAATGAGAAATGAGAAATGAGAAATGAG 1344
QY 1321 ACCACTCTAATCAAGAAAGAAATTAACAGCTGATTTCACTGATGATTTGAATCTAA 1380
DB 1345 ACCACTCTAATCAAGAAAGAAATTAACAGCTGATTTCACTGATGATTTGAATCTAA 1404
QY 1381 AAATGTTATCATTAAGGCTTTGATTTAATAAATTTGGGTACTATTAATAATATAG 1440
DB 1405 AAATGTTATCATTAAGGCTTTGATTTAATAAATTTGGGTACTATTAATAATATAG 1464
QY 1441 TAGTTATCTGCTTCCAGTTGCTGATATATTTGTTGATTAAGATTTCTGACTTAT 1500
DB 1465 TAGTTATCTGCTTCCAGTTGCTGATATATTTGTTGATTAAGATTTCTGACTTAT 1524
QY 1501 ATTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACAT 1560
DB 1525 ATTTGAATGGTCTAGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACAT 1584
QY 1561 TATTTACACTCTGATTTCAATGATGAAATGAGAAATGAGAAATGAGAAATGAGTGA 1620
DB 1585 TATTTACACTCTGATTTCAATGATGAAATGAGAAATGAGAAATGAGAAATGAGTGA 1644
QY 1621 TAAAGTCAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1645 TAAAGTCAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1704
QY 1681 ATCTCCCTTAAGCAGATTTCAAACTTTAGCAACAGTTATCAACATTTGTAATTTGCAAA 1740
DB 1705 ATCTCCCTTAAGCAGATTTCAAACTTTAGCAACAGTTATCAACATTTGTAATTTGCAAA 1764
QY 1741 GAAAAGTTTCACTGATTTAATCAAGATGCTTCAACTTAATAAATAATTAATAAATA 1800
DB 1765 GAAAAGTTTCACTGATTTAATCAAGATGCTTCAACTTAATAAATAATTAATAAATA 1824
QY 1801 ATGAGGAATGTGTGGCTACTAGAGAGTGCAGAGGAGACAGTCACTTTAGGGTGC 1860


```
Db 1825 ATGAGAAATGCTGGCTCACTACAGTAGAGTCCAGAGGACAGTCACTTTAGGGTTGC 1884
Qy 1861 CTGTATTCAGTAAGTACGAGGAGGCTGTTTCCCGGTGGGTCTCTGAGCTTTCCTTT 1920
Db 1885 CTGTATTCAGTAAGTACGAGGAGGCTGTTTCCCGGTGGGTCTCTGAGCTTTCCTTT 1944
Qy 1921 CTGTATTCAGTAAGTACGAGGAGGCTGTTTCCCGGTGGGTCTCTGAGCTTTCCTTT 1980
Db 1945 CTGTATTCAGTAAGTACGAGGAGGCTGTTTCCCGGTGGGTCTCTGAGCTTTCCTTT 2004
Qy 1981 CAGCAATCCAGAAATTAAGTTCT 2005
Db 2005 CAGCAATCCAGAAATTAAGTTCT 2029

RESULT 4
US-09-967-305-8
: Sequence 8: Application us/09967305
: Patient No. US20020123081A1
: GENERAL INFORMATION:
: APPLICANT: Richardson, Jennifer
: APPLICANT: Monahan, John
: TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
: FILE REFERENCE: 07334-312001
: CURRENT APPLICATION NUMBER: US/09/967,305
: PRIOR FILING DATE: 2001-09-28
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 3023
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (90)...(683)
US-09-967-305-8

Query Match 83.4% Score 1671.4: DB 10: Length 3023:
Best Local Similarity 91.9% Pred. No. 0:
Matches 1843: Conservative 0: Mismatches 1: Indels 161: Gaps 1:

Qy 1 TTCGAGGCTGTGGGCTGGGCTAAGGCTGCTCAGTTTCCTTACGCGGGCAGCTGGGAA 60
Db 25 TTCGAGGCTGTGGGCTGGGCTAAGGCTGCTCAGTTTCCTTACGCGGGCAGCTGGGAA 84
Qy 61 GCGCATGAGCTGAGGAGGCACTCGGTGAGAGTGTCCGGCTGGCCCGGCGCCGT 120
Db 85 GCGCATGAGCTGAGGAGGCACTCGGTGAGAGTGTCCGGCTGGCCCGGCGCCGT 144
Qy 121 TCTGTGCTATGCTGTGGCTGACTTTCGGGCGGCTGTGGTAGCGCTGGACCGGCGCT 180
Db 145 TCTGTGCTATGCTGTGGCTGACTTTCGGGCGGCTGTGGTAGCGCTGGACCGGCGCT 204
Qy 181 CCGGCTAGACGCTGAGGCGCTTGGGCGGCGGCAAGCGCTCGTAGTGTGAGCTGAGAGC 240
Db 205 CCGGCTAGACGCTGAGGCGCTTGGGCGGCGGCAAGCGCTCGTAGTGTGAGCTGAGAGC 264
Qy 241 AGCGGGGGGAGCGCGCTGCTGGCGGCTGTGTGCAAGCGGTGGATGTGTGCTGGAGC 300
Db 265 AGCGGGGGGAGCGCGCTGCTGGCGGCTGTGTGCAAGCGGTGGATGTGTGCTGGAGC 324
Qy 301 CTTTCGCGCGGCTGTATGAGAACTCCAGCTGGGCGCCAGAGATTTCGACGCGGAAA 360
Db 325 CTTTCGCGCGGCTGTATGAGAACTCCAGCTGGGCGCCAGAGATTTCGACGCGGAAA 384
Qy 361 ATCCAGGCTTATTTATGCGCAGGCTGAGTGTGATTTGGCCAGTACAGAACTTTCGCGGT 420
Db 385 ATCCAGGCTTATTTATGCGCAGGCTGAGTGTGATTTGGCCAGTACAGAACTTTCGCGGT 444
Qy 421 TAGCTGGCGAGATATCAACTATTTGGCTTTCAGAGGTGTTCTCTCAAAATTTGCGAGAA 480
```

```
Db 445 TAGCTGGCGAGATATCAACTATTTGGCTTTCAGAGGTGTTCTCTCAAAATTTGCGAGAA 479
Qy 481 GTGTGAGAAATCCGATATGCGCGCGGCAATCTCGGCTGACTTTCGCTGGGTGGCTTTA 540
Db 480 ----- 479
Qy 541 TGTTGCACTGGGCAATTATATGCTTTTGTACCGCACACGACGCAAGGTCAGG 600
Db 480 ----- 479
Qy 601 TCATGATGCAAAATATGTTGGAAGGAAACAGCATTTTAACTTTTCTGTGAAAATC 660
Db 480 -----GTTGGAAGGAAACAGCATTTTAACTTTTCTGTGAAAATC 523
Qy 661 AGAAATGAGTCTGTGGGAGAGCACTCGAGAGCAAACTGTGATGGTGGAGAGACCTT 720
Db 524 AGAAATGAGTCTGTGGGAGAGCACTCGAGAGCAAACTGTGATGGTGGAGAGACCTT 583
Qy 721 TCTATGCACTTACAGAGACAGATGGGAACTTCACTGCTGTGGAGCAATAGAACCC 780
Db 584 TCTATGCACTTACAGAGACAGATGGGAACTTCACTGCTGTGGAGCAATAGAACCC 643
Qy 781 AGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTGTGATGAACTTCCCAATCAGA 840
Db 644 AGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTGTGATGAACTTCCCAATCAGA 703
Qy 841 TGAGCATGATGATGTTGGCCAGAAATGAAGAAGATTGCGAGATATTTGCAAGAAGA 900
Db 704 TGAGCATGATGATGTTGGCCAGAAATGAAGAAGATTGCGAGATATTTGCAAGAAGA 763
Qy 901 CGAAGGAGAGTGTGTTCAAACTTTGAGGAGCAGATGCTGTGAGTCCGCTTCTGA 960
Db 764 CGAAGGAGAGTGTGTTCAAACTTTGAGGAGCAGATGCTGTGAGTCCGCTTCTGA 823
Qy 961 CTTTGGAGAGTGTGTTCAAACTTTGAGGAGCAGATGCTGTGAGTCCGCTTCTGA 1020
Db 824 CTTTGGAGAGTGTGTTCAAACTTTGAGGAGCAGATGCTGTGAGTCCGCTTCTGA 883
Qy 1021 AGAGAGCAGAGCTGAGCCCGCCCGCTGCACTTCTGTGTTAAACACCCAGCCATCCCTT 1080
Db 884 AGAGAGCAGAGCTGAGCCCGCCCGCTGCACTTCTGTGTTAAACACCCAGCCATCCCTT 943
Qy 1081 CTTTCAAAAGGATCTTTCATAGAGAAACACAGTGAAGATTAAGTGAATTTGGAT 1140
Db 944 CTTTCAAAAGGATCTTTCATAGAGAAACACAGTGAAGATTAAGTGAATTTGGAT 1003
Qy 1141 TCAGCCGCGAAGAGATTTATCAGCTTAAGTAAATCATTTGAAGTAAATTAAGTTAA 1200
Db 1004 TCAGCCGCGAAGAGATTTATCAGCTTAAGTAAATCATTTGAAGTAAATTAAGTTAA 1063
Qy 1201 AAGCTAGTCTTAACTTCAGGCGCCAGGCTCAAGTGAATTTGAATTAAGTAACTTAACT 1260
Db 1064 AAGCTAGTCTTAACTTCAGGCGCCAGGCTCAAGTGAATTTGAATTAAGTAACTTAACT 1123
Qy 1261 GTAGAGTAACATTAATGATGATGATGAGAAATGAGAGATTAAGTAACTTAACTTAACT 1320
Db 1124 GTAGAGTAACATTAATGATGATGATGAGAAATGAGAGATTAAGTAACTTAACTTAACT 1183
Qy 1321 ACACCTTAATCAAGAAAGATTTACAGACTGTGATTTCTACAGTATGATTAATTTAA 1380
Db 1184 ACACCTTAATCAAGAAAGATTTACAGACTGTGATTTCTACAGTATGATTAATTTAA 1243
Qy 1381 AATGATGATCAATAGGCTTTGATTTATTAATTAATTAATTAATTAATTAATTAATG 1440
Db 1244 AATGATGATCAATAGGCTTTGATTTATTAATTAATTAATTAATTAATTAATTAATG 1303
Qy 1441 TAGTTATTTGCTTCACTTGTGATTAATTTGTTGATTAATTAAGATTTTGAATTTAT 1500
Db 1304 TAGTTATTTGCTTCACTTGTGATTAATTTGTTGATTAATTAAGATTTTGAATTTAT 1363
Qy 1501 ATTTGATGAGTGTGAGAAAGAAATGATATTTCTTGAAGCATCGATATACATTT 1560
```

Db 1364 ATTTTGAATGGGCTTCTAGTGAAGAAAAAGATATATTTCTTGAAGACATCATATACATT 1423
QY 1561 TATTTACACTCTTGATTTCTACATATGTAGAAATGAGAAATGCCACAATTTGATGTGA 1620
Db 1424 TATTTACACTCTTGATTTCTACATATGTAGAAATGAGAAATGCCACAATTTGATGTGA 1483
QY 1621 TAAAAAGTCAGTGAAGACAGAGTGTGTCATCCAGGCGCTTTTGTCTGTGTTGATG 1680
Db 1484 TAAAAAGTCAGTGAAGACAGAGTGTGTCATCCAGGCGCTTTTGTCTGTGTTGATG 1543
QY 1681 ATCTCCCTTAAGACACATTTCCAACTTTAGCAAGTATTCACACTTTGTATTTGCAAA 1740
Db 1544 ATCTCCCTTAAGACACATTTCCAACTTTAGCAAGTATTCACACTTTGTATTTGCAAA 1603
QY 1741 GAAAAGTTTACCTGTATTTGATGAGATGCTTCAACTGAAAAAAACATATCCAAATA 1800
Db 1604 GAAAAGTTTACCTGTATTTGATGAGATGCTTCAACTGAAAAAAACATATCCAAATA 1663
QY 1801 ATGAGAAATGTGTGCTCCTACGTAGAGTCCAGAGGACAGTCAAGTTTAAAGGTTGC 1860
Db 1664 ATGAGAAATGTGTGCTCCTACGTAGAGTCCAGAGGACAGTCAAGTTTAAAGGTTGC 1723
QY 1861 CTGTATCCAGTAACTGGGGGCTGTTCCCGTGGGTCTCTGGGCTGTCACTTCTCTT 1920
Db 1724 CTGTATCCAGTAACTGGGGGCTGTTCCCGTGGGTCTCTGGGCTGTCACTTCTCTT 1783
QY 1921 CTCCATGTGTTTGAATTTCTCTCAGGCTGTGAGCAAGTTCTGATCTTATACCAACACA 1980
Db 1784 CTCCATGTGTTTGAATTTCTCTCAGGCTGTGAGCAAGTTCTGATCTTATACCAACACA 1843
QY 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
Db 1844 CAGCAACATCCAGAAATTAAGATCT 1868

RESULT 5
US-09-232-880-107
; Sequence 107, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232.880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ. ID NOS: 338
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-107

Query Match 78.5%; Score 1574.2; DB 9; Length 1621;
Best local similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGAGAGGCACTCGGTCGTGAGACTGTCCGGCCCTGGCCCGCCCGCTT 121
Db 1 CGCCATGGCACTGAGAGGCACTCGGTCGTGAGACTGTCCGGCCCTGGCCCGCCCGCTT 60
QY 122 CTGTGATGATGCTGCTGCTGACTCGGGGGCGCTGTGTAGCGGTGACGCGCCGGGCTC 181
Db 61 CTGTGATGATGCTGCTGCTGACTCGGGGGCGCTGTGTAGCGGTGACGCGCCGGGCTC 120
QY 182 CCGCTAGACGTGAGCCGCTTGGCCGCGGCAACGCGCTCGCTAGTGTGACCTGAAGCA 241
Db 121 CCGCTAGACGTGAGCCGCTTGGCCGCGGCAACGCGCTCGCTAGTGTGACCTGAAGCA 180
QY 242 GCCGCGGAGAGCCGCCGCTGTGCGCGGCTGTGTGCAAGCGGTGATGTGCTGAGACC 301

Db 181 GCCCGGGGAGCCGCCGTGCTGGCGCTGTGTGCAACGGGTGGATGTGCTGTGGAGCC 240
QY 302 CTTCCGGCGGGGTGATGAGAAATCTCAGCTGGGCCAGAGATTTGCGAGCGGAAAA 361
Db 241 CTTCCGGCGGGGTGATGAGAAATCTCAGCTGGGCCAGAGATTTGCGAGCGGAAAA 300
QY 362 TCCAGGCTTATTTATGTCAGAGGCTGAGTGTGATTTGGCCAGTCAAGAGCTTGTCCGGTT 421
Db 301 TCCAGGCTTATTTATGTCAGAGGCTGAGTGTGATTTGGCCAGTCAAGAGCTTGTCCGGTT 360
QY 422 AGCTGGCCAGATATCAACTATTTGGCTTGTGAGGTTCTCTCAAAATTTGGCAAG 481
Db 361 AGCTGGCCAGATATCAACTATTTGGCTTGTGAGGTTCTCTCAAAATTTGGCAAG 420
QY 482 TGTGAGAAATCCGTATCCCGGCTGAATCTCTGCTGACTTTGCTGGTGGCTTAT 541
Db 421 TGTGAGAAATCCGTATCCCGGCTGAATCTCTGCTGACTTTGCTGGTGGCTTAT 480
QY 542 GTGTGCACTGGGCATTTATATGCTCTTTTGAACCGACACGCACTGGCAAGGTCAGT 601
Db 481 GTGTGCACTGGGCATTTATATGCTCTTTTGAACCGACACGCACTGGCAAGGTCAGT 540
QY 602 CATTCATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAAGACTCA 661
Db 541 CATTCATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAAGACTCA 600
QY 662 GAAATCGAGTCTGTGGAGACACCTCGAGACAGCAAGATGTTGGATGGAGACCTTT 721
Db 601 GAAATCGAGTCTGTGGAGAGACCTCGAGAGCACAACATGTTGATGTTGGAGACCTTT 660
QY 722 CTATAGCACTTACAGACAGCAGATGGGGAATTTATGCTGTTGGACATAGAACCCCA 781
Db 661 CTATAGCACTTACAGACAGCAGATGGGGAATTTATGCTGTTGGACATAGAACCCCA 720
QY 782 GTTCTAGAGCTGCTGATTCAAAGAGCTTGGACTAAGTCTGATGAATCTTCCAAATCAGAT 841
Db 721 GTTCTAGAGCTGCTGATTCAAAGAGCTTGGACTAAGTCTGATGAATCTTCCAAATCAGAT 780
QY 842 GAGCATGGATGATTTGGCCAGAAATGAAGAAAGATTTGCAAGATGATTTTGCAGAAAGAC 901
Db 781 GAGCATGGATGATTTGGCCAGAAATGAAGAAAGATTTGCAAGATGATTTTGCAGAAAGAC 840
QY 902 GAAGCAGAGTGTGCTCAAAATCTTTGACGCGACAGATGCTGTGACTCCGGTTCTGAC 961
Db 841 GAAGCAGAGTGTGCTCAAAATCTTTGACGCGACAGATGCTGTGACTCCGGTTCTGAC 900
QY 962 TTTTGAGAGGTTGTTTCATCATGATCAACCAAGAAAGGGGCTGCTTTATCACACAGTGA 1021
Db 901 TTTTGAGAGGTTGTTTCATCATGATCAACCAAGAAAGGGGCTGCTTTATCACACAGTGA 960
QY 1022 GGAGCAGAGCTGAGCCGCCGCCCTGACCTCTGCTTTAAACACCCAGCATCCCTTC 1081
Db 961 GGAGCAGAGCTGAGCCGCCGCCCTGACCTCTGCTTTAAACACCCAGCATCCCTTC 1020
QY 1082 TTTTCAAAAAGGATCTTTTCATAGAGAACAACACTGAGAGATTAATTAAGATTTGGATTT 1141
Db 1021 TTTTCAAAAAGGATCTTTTCATAGAGAACAACACTGAGAGATTAATTAAGATTTGGATTT 1080
QY 1142 CAGCCGCGAAGAGATTTATTCAGCTTAACATCAAGATTAATCACTTGAAGTAAATAGTAAA 1201
Db 1081 CAGCCGCGAAGAGATTTATTCAGCTTAACATCAAGATTAATCACTTGAAGTAAATAGTAAA 1140
QY 1202 AGCTAGTCTCTAATCTCCAGGCCACAGGCTCAAGTGAATTTGAATTAATCTGATTTACAGTG 1261
Db 1141 AGCTAGTCTCTAATCTCCAGGCCACAGGCTCAAGTGAATTTGAATTAATCTGATTTACAGTG 1200
QY 1262 TAGAGTAACACATTAATGATGATGAAGAAACATGAGAAACGATATTACAGTGTCTTA 1321
Db 1201 TAGAGTAACACATTAATGATGATGAAGAAACATGAGAAACGATATTACAGTGTCTTA 1260
QY 1322 CCACTCTAATTCAGAAAGAAATTAACAGCTCTGATTTCTACAGTGATGATTAATTTCAAA 1381
Db 1322 CCACTCTAATTCAGAAAGAAATTAACAGCTCTGATTTCTACAGTGATGATTAATTTCAAA 1381

Db 1261 CCACTCTAATCAAGAAAGATTTACACACTCTGATTTCTACAGTGATGATTTGATTTAA 1320
 Qy 1382 AATGTTATCATATGAGCGTTTGTATTAATAAAGTTGGTACTATTAATAATATATGTT 1441
 Db 1321 AATGTTATCATATGAGCGTTTGTATTAATAAAGTTGGTACTATTAATAATATATGTT 1380
 Qy 1442 AGTTATTCGCTTCCATGTTGCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1501
 Db 1381 AGTTATTCGCTTCCATGTTGCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440
 Qy 1502 TTTTGAATGGTTCATGTAAGAAAGATGATATATTTCTTGAAGACATGATATACATTT 1561
 Db 1441 TTTTGAATGGTTCATGTAAGAAAGATGATATATTTCTTGAAGACATGATATACATTT 1500
 Qy 1562 ATTTACAGCTTGATTTGATACAAATGAGAAATGAGAAATGACAAATGATGATGAT 1621
 Db 1501 ATTTACAGCTTGATTTGATACAAATGAGAAATGAGAAATGACAAATGATGATGAT 1560
 Qy 1622 AAAAGTCAGCTGAACACGA 1640
 Db 1561 AAAAGTCAGCTGAACACGA 1579

RESULT 6

US-10-012-896-107
 : Sequence 107, Application US/10012896
 : Publication NO. US20020183251A1

GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, Davin C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yugu
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: Retter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Carter, Darick
 : APPLICANT: Li, Samuel X.
 : APPLICANT: Wang, Aljun
 : APPLICANT: Skeiky, Rasit A.W.
 : APPLICANT: Hepler, William F.
 : APPLICANT: Henderson, Robert A.
 : APPLICANT: Hurai, John
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Houghton, Raymond L.
 : APPLICANT: Vinals de Bassols, Carlota
 : APPLICANT: Foy, Teresa
 : APPLICANT: Fanger, Gary R.
 : APPLICANT: Wantanabe, Yoshihiro
 : APPLICANT: Meagher, Madeleine Joy
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 : FILE REFERENCE: 210121.427C27
 : CURRENT APPLICATION NUMBER: US/10/012.896
 : NUMBER OF SEQ ID NOS: 2001-12-10
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 107
 : LENGTH: 1621
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-10-012-896-107

Query Match 78.5%; Score 1574.2; DB 9; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 62 CGCCATGCGACTGCGAGGCGATCTCGTCTGAGAGCTGTCGCGGCTGCGCCGCGCGCGTT 121
 Db 1 CGCCATGCGACTGCGAGGCGATCTCGTCTGAGAGCTGTCGCGGCTGCGCCGCGCGCGTT 60

Qy 122 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 Db 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Qy 182 CGCTACGACGTGACCGCTTGGGCGCGGGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 Db 121 CGCTACGACGTGACCGCTTGGGCGCGGGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 Qy 242 GCGCGGGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
 Db 181 GCGCGGGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Qy 302 CTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
 Db 241 CTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Qy 362 TCCAGGCTATTTATGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 Db 301 TCCAGGCTATTTATGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Qy 422 AGCTGGCGACGATATCAACTTTTGGCTTGTACAGGTGTTCTCAAAAATTTGGCAGAG 481
 Db 361 AGCTGGCGACGATATCAACTTTTGGCTTGTACAGGTGTTCTCAAAAATTTGGCAGAG 420
 Qy 482 TGCTGAGAAATCCGTAATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
 Db 421 TGCTGAGAAATCCGTAATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Qy 542 GTGTGCACTGGGCTATTAATGAGTCTTTTGGACGCGACACGCTGCGCAAGGGTCAAGT 601
 Db 481 GTGTGCACTGGGCTATTAATGAGTCTTTTGGACGCGACACGCTGCGCAAGGGTCAAGT 540
 Qy 602 CATTTGATGCAAAATATGCGGAGGAGAACAGCATTTTAAGTCTTTTCTGCGGAAACTCA 661
 Db 541 CATTTGATGCAAAATATGCGGAGGAGAACAGCATTTTAAGTCTTTTCTGCGGAAACTCA 600
 Qy 662 GAAATGAGTCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 721
 Db 601 GAAATGAGTCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 Qy 722 CTATACGACTTACAGGACGACGATGGGGAATTCATGCTGTTGGAGCAATGAACCCCA 781
 Db 661 CTATACGACTTACAGGACGACGATGGGGAATTCATGCTGTTGGAGCAATGAACCCCA 720
 Qy 782 GTTCTACGAGTGTGATCAAAAGGACTTGGACTTGAATGTAAGTCTGATGAACTTCCCAATCAGAT 841
 Db 721 GTTCTACGAGTGTGATCAAAAGGACTTGGACTTGAATGTAAGTCTGATGAACTTCCCAATCAGAT 780
 Qy 842 GACATGATGATGATGGCCAGAAATGAAGAAGATTGCGAGATGTAATTTGCAAGAAGAC 901
 Db 781 GACATGATGATGATGGCCAGAAATGAAGAAGATTGCGAGATGTAATTTGCAAGAAGAC 840
 Qy 902 GAGGCGAGGCTGTCAAAATCTTTGACGCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
 Db 841 GAGGCGAGGCTGTCAAAATCTTTGACGCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Qy 962 TTTTGGAGGCTTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
 Db 901 TTTTGGAGGCTTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Qy 1022 GAGGCGAGGCTGTCAAAATCTTTGACGCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
 Db 961 GAGGCGAGGCTGTCAAAATCTTTGACGCGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Qy 1082 TTTCAAAAGGATCTTTTCAATGAGGAGACACTGAGGAGATCTTGAAGATTTGGATT 1141
 Db 1021 TTTCAAAAGGATCTTTTCAATGAGGAGACACTGAGGAGATCTTGAAGATTTGGATT 1080
 Qy 1142 CAGCGCGAGGAGATTTATCAGCTTAACTGATTAATAATCATTTGAAGATTAAGTAA 1201
 Db 1081 CAGCGCGAGGAGATTTATCAGCTTAACTGATTAATAATCATTTGAAGATTAAGTAA 1140
 Qy 1202 AGCTAGTCTTAATCTTCAAGGCGGCTCAAGTGAATTTGAATGATGATTTGATTAAGTG 1261

```

|||||
Db 1141 AGCTAGTCTCTACTTCCAGGGCCACGGCTCAAGTGAATTTGAATCTGATTTACAGTG 1200
Qy 1262 TAGAGTAACACATACATATGATGATGAGAAACATGAGAAACAGATTTACAGTGCCTA 1321
Db 1201 TAGAGTAACACATACATATGATGATGAGAAACATGAGAAACAGATTTACAGTGCCTA 1260
Qy 1322 CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAAATTTCAAA 1381
Db 1261 CCACCTTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTGAATGAAATTTCAAA 1320
Qy 1382 AAGGTATCATATGAGGCTTTTATTTAAACCTTGGTACTTATACAAATTTATGCT 1441
Db 1321 AAGGTATCATATGAGGCTTTTATTTAAACCTTGGTACTTATACAAATTTATGCT 1380
Qy 1442 AGTATATTCGCCCTTCCAGTTTGCTGATATATTTGTTGATTTAAATCTTGACTTAA 1501
Db 1381 AGTATATTCGCCCTTCCAGTTTGCTGATATATTTGTTGATTTAAATCTTGACTTAA 1440
Qy 1502 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTTGAAGACATGATATACATTT 1561
Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTTGAAGACATGATATACATTT 1500
Qy 1562 ATTATACACTCTGATCTCAATGTAGAAATGAGAAATGCCAAATTTGTATGGTGA 1621
Db 1501 ATTATACACTCTGATCTCAATGTAGAAATGAGAAATGCCAAATTTGTATGGTGA 1560
Qy 1622 AAAAGTCACGTGAACAGA 1640
Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 7
US-09-895-793-107
; Sequence 107, Application US/09895793
; Publication No. US20020192763A1.
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: Fasted for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-107
Query Match 78.5%; Score 1574.2; DB 9; Length 1621;

```

```

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 62 CGCCATGACACATCAGGAGCATCTGCTGAGAGCTGTCCGGCTGGCCCGCCGGCCGTT 121
Db 1 CGCCATGACACATCAGGAGCATCTGCTGAGAGCTGTCCGGCTGGCCCGCCGGCCGTT 60
Qy 122 CTGTGTATGCTCTGCTGACTCTGGGGGCGCTGTGTATGCTGTGAGACCGCCGGCTC 181
Db 61 CTGTGTATGCTCTGCTGACTCTGGGGGCGCTGTGTATGCTGTGAGACCGCCGGCTC 120
Qy 182 CGCCTACGACGTGAGCGCTGGGGCGGGCAAGCGCTGCTGTGCTGTGACCTGAAGCA 241
Db 121 CGCCTACGACGTGAGCGCTGGGGCGGGCAAGCGCTGCTGTGCTGTGACCTGAAGCA 180
Qy 242 GCGCGGGGAGCGCGCGCTGCTGGGGGCTGTGTCAAGCGCTGCGATGTGCTGTGAGCC 301
Db 181 GCGCGGGGAGCGCGCGCTGCTGGGGGCTGTGTCAAGCGCTGCGATGTGCTGTGAGCC 240
Qy 302 CTTCGCCCGCGGCTGTATGAGAGAACTCCAGCTGGGCCCAAGATTTCTGACGGGAAAA 361
Db 241 CTTCGCCCGCGGCTGTATGAGAGAACTCCAGCTGGGCCCAAGATTTCTGACGGGAAAA 300
Qy 362 TCCAAAGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCCAGAGCTTGTGCCGCTT 421
Db 301 TCCAAAGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCCAGAGCTTGTGCCGCTT 360
Qy 422 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGAG 481
Db 361 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGAG 420
Qy 482 TGGTGAGATCCGTATGCCCGCGCTGAATCTCCCTGCTGACTTGTCTGTGTGGCCCTTAT 541
Db 421 TGGTGAGATCCGTATGCCCGCGCTGAATCTCCCTGCTGACTTGTCTGTGTGGCCCTTAT 480
Qy 542 GTGTGACTGGGCTATATATGCTCTTTTGTGCCACACGACTGGCAAGGCTCAGGT 601
Db 481 GTGTGACTGGGCTATATATGCTCTTTTGTGCCACACGACTGGCAAGGCTCAGGT 540
Qy 602 CATTGATGCMAATATGCTGGAAGAGACAGATATTTAACTCTTTCTGTGAAAACCTCA 661
Db 541 CATTGATGCMAATATGCTGGAAGAGACAGATATTTAACTCTTTCTGTGAAAACCTCA 600
Qy 662 GAATGAGTCTGTGGGAAGACCTCGAGACAGAACTGTGTGATGTGTGAGACACTTT 721
Db 601 GAATGAGTCTGTGGGAAGACCTCGAGACAGAACTGTGTGATGTGTGAGACACTTT 660
Qy 722 CTATAGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCA 781
Db 661 CTATAGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCA 720
Qy 782 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCAAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCAAATCAGAT 780
Qy 842 GAGCATGATGATTTGCCCGAAATGAAGAAAGTTTGCAGATGTATTTGCCAAAGAAAGC 901
Db 781 GAGCATGATGATTTGCCCGAAATGAAGAAAGTTTGCAGATGTATTTGCCAAAGAAAGC 840
Qy 902 GAAGGAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTACTCCGGTTGTGAC 961
Db 841 GAAGGAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTACTCCGGTTGTGAC 900
Qy 962 TTTTGAAGAGTTGTTCATCATGATCAACAAGAGAGGGGCTGTTTATCAACAGTGA 1021
Db 901 TTTTGAAGAGTTGTTCATCATGATCAACAAGAGAGGGGCTGTTTATCAACAGTGA 960
Qy 1022 GGAAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTAACACCCACCATCCCTTC 1081
Db 961 GGAAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTAACACCCACCATCCCTTC 1020
Qy 1082 TTTCAAAAGGATCTTTTATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1141
Db 1082 TTTCAAAAGGATCTTTTATAGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATT 1141

```


QY	1022	GGACGACGACGTAGACCCCGCCGCTCAGCTCGCTGTAAACACCCGACCATCCCTTC	1081
Db	961	GGAGCAGGACGTAGGCCCGCCGCTCAGCTCGCTGTAAACACCCGACCATCCCTTC	1020
QY	1082	TTTCAAAAGGAGATCCTTTCATATAGAGAACACACTGAGAGATCTTGAAGAAATTTGGATT	1141
Db	1021	TTTCAAAAGGAGATCCTTTCATATAGAGAACACACTGAGAGATCTTGAAGAAATTTGGATT	1080
QY	1142	CAGCCCGGAAGAGATTTATAGCTTTAATCAATGATTAATCATTTGAAGATTAATAGGTAAA	1201
Db	1081	CAGCCCGGAAGAGATTTATAGCTTTAATCAATGATTAATCATTTGAAGATTAATAGGTAAA	1140
QY	1202	AGCTAGTCTCTAACCTTTCAGAGCCGACGGCTCAAGTGAATTTGAATCACTTTCAGGTG	1261
Db	1141	AGCTAGTCTCTAACCTTTCAGAGCCGACGGCTCAAGTGAATTTGAATCACTTTCAGGTG	1200
QY	1262	TAGAGTAACACATTAACATTTGTATGCATGGAACATGAGGAACAGATTAATACAGTGCCTA	1321
Db	1201	TAGAGTAACACATTAACATTTGTATGCATGGAACATGAGGAACAGATTAATACAGTGCCTA	1260
QY	1322	CCACTCTAATCAAGAAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTGAATTTCTAAA	1381
Db	1261	CCACTCTAATCAAGAAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTGAATTTCTAAA	1320
QY	1382	AATGTTATCATTAAGGCGCTTTTATTTATTAACCTTTGGGTACTATACATAATATATGCT	1441
Db	1321	AATGTTATCATTAAGGCGCTTTTATTTATTAACCTTTGGGTACTATACATAATATATGCT	1380
QY	1442	AGTTATTTCTCCCTTCAGATTTCCTGATATATTTGTTGATTAATTAAGATTCTTGACTTTATA	1501
Db	1381	AGTTATTTCTCCCTTCAGATTTCCTGATATATTTGTTGATTAATTAAGATTCTTGACTTTATA	1440
QY	1502	TTTTGATATGGGTTCTACTGAAAAGAAATGATATATTTCTTGAAGACATCGAATATCAATT	1561
Db	1441	TTTTGATATGGGTTCTACTGAAAAGAAATGATATATTTCTTGAAGACATCGAATATCAATT	1500
QY	1562	ATTTACACTCTTGATCTCTACAAATGTAGAAAATGAGAAATGCCACAATTTGATGCTGAT	1621
Db	1501	ATTTACACTCTTGATCTCTACAAATGTAGAAAATGAGAAATGCCACAATTTGATGCTGAT	1560
QY	1622	AAAAGTCACGTGAACAGCA 1640	
Db	1561	AAAAGTCACGTGAACAGCA 1579	
RESULT 9			
US-09-759-143-107			
: Sequence 107, Application US/09759143			
: Patent No. US200202248A1			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jjiang, Yuqul			
: APPLICANT: Henderson, Robert A.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retter, Marc W.			
: APPLICANT: Stolk, John A.			
: APPLICANT: Day, Craiy H.			
: APPLICANT: Vedvick, Thomas S.			
: APPLICANT: Carter, Darrick			
: APPLICANT: Li, Samuel			
: APPLICANT: Wang, Aljun			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Hepler, William			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
: FILE REFERENCE: 210121.427C23			
: CURRENT APPLICATION NUMBER: US/09/759,143			
: CURRENT FILING DATE: 2001-01-12			

```

: NUMBER OF SEQ ID NOS: 934
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 107
: LENGTH: 1621
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-759-143-107

Query Match      78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      62  CGCCATGGCACTGCAAGGGGCACTCGGTCGTGGAGCTGTCCGGCCCTGGCCCGGCGCGTT 121
Db      1  CGCCATGGCACTGCAAGGGGCACTCGGTCATGAGAGCTGTCCGGCCCTGGCCCGGCGCGTT 60

QY      122 CTGTGCTATGCTCTCGCTGACTTCGGGGCCGTCGTGGTACGGCTGGAGCCGGCCCGGCTC 181
Db      61 CTGTGCTATGCTCTCGCTGACTTCGGGGCCGTCGTGGTACGGCTGGAGCCGGCCCGGCTC 120

QY      182 CCGCTACGACGTGAGACCCCTTGGGCGCGGGGCAAGCGCTCGCTAGTGTGAGACTTGAACA 241
Db      121 CCGCTACGACGTGAGACCCCTTGGGCGCGGGGCAAGCGCTCGCTAGTGTGAGACTTGAACA 180

QY      242 GCCCGGGGGAGCCGCGCTGTCTGGCGGCGTCTGTGCAAGCGGTGGATGTGTGTCTGGAGCC 301
Db      181 GCCCGGGGGAGCCGCGCTGTCTGGCGGCGTCTGTGCAAGCGGTGGATGTGTCTGTGGAGCC 240

QY      302 CTTCGCGCGCGGTGTCATGAGAAACCTCAGCTGGGCGCCAGAGATTTGCAAGCGGGAAAA 361
Db      241 CTTCGCGCGCGGTGTCATGAGAAACCTCAGCTGGGCGCCAGAGATTTCTGACAGCGGAAAA 300

QY      362 TCACAAGGCTTATTTATGCGCAGGCTGAGTGATTTTGGCCAGTCAGGAAGCTTCTGCGGTT 421
Db      301 TCACAAGGCTTATTTATGCGCAGGCTGAGTGAGTTTGGCCAGTCAGGAAGCTTCTGCGGTT 360

QY      422 AGCTGGCCACATATCAACTATTTGGCTTTGTGCAAGCTTCTTCAAAAATTTGGCAGAG 481
Db      361 AGCTGGCCACATATCAACTATTTGGCTTTGTGCAAGCTTCTTCAAAAATTTGGCAGAG 420

QY      482 TGGTGAGAAATCCGTAATGCCCGCTGAAATCCTCGCTACTTTGCTGGTGGGCGCTTAT 541
Db      421 TGGTGAGAAATCCGTAATGCCCGCTGAAATCCTCGCTACTTTGCTGGTGGGCGCTTAT 480

QY      542 GTGTGACTGGGCATTTAATAGGCTCTTTTGTGACCGCACAGCACTGGCAGAGGCTCAGT 601
Db      481 GTGTGACTGGGCATTTAATAGGCTCTTTTGTGACCGCACAGCACTGGCAGAGGCTCAGT 540

QY      602 CATTGATCAAAATATGTTGGGAAGAACAGCATATTTAGTCTCTTTTCTGTGGAAAACTCA 661
Db      541 CATTGATCAAAATATGTTGGGAAGAACAGCATATTTAGTCTCTTTTCTGTGGAAAACTCA 600

QY      662 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 721
Db      601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660

QY      722 CTATACGACTTACAGGAACAGAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCTCA 781
Db      661 CTATACGACTTACAGGAACAGAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCTCA 720

QY      782 GTTCTACAGAGCTGTGATCAAGAAGCACTTGAATAAGTCTGATGAACCTTCCCAATCAGAT 841
Db      721 GTTCTACAGAGCTGTGATCAAGAAGCACTTGAATAAGTCTGATGAACCTTCCCAATCAGAT 780

QY      842 GAGCATGATATATTGGCCAGAAATGAGAAAGTTTCCAGATGTATTTGGCAAGAAAGAC 901
Db      781 GAGCATGATATATTGGCCAGAAATGAGAAAGTTTCCAGATGTATTTGGCAAGAAAGAC 840

QY      902 GAAGGACAGATGGGTCAAAATCTTTGAGGGGACAGATCCTGTGTGACTCCGGTCTGAC 961
Db      841 GAAGGACAGATGGGTCAAAATCTTTGAGGGGACAGATCCTGTGTGACTCCGGTCTGAC 900

QY      962 TTTTGGAGGAGGTGTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGA 1021

```

[illegible]

QY	902	GAAGGCAGAGTGTGCTCAAAATCTTTGAGGGCAGACATGCGCTGTGACTCCGGTCTGAC	961
Db	841	GAAGGCAGAGTGTGCTCAAAATCTTTGAGGGCAGACATGCGCTGTGACTCCGGTCTGAC	900
QY	962	TTTTGAGGAGGTTGTTCAATCATGATCACACACAGAGAGGGGGCTGTTTATCACCAGTGA	1021
Db	901	TTTTGAGGAGGTTGTTCAATCATGATCACACACAGAGAGGGGGCTGTTTATCACCAGTGA	960
QY	1022	GGAGCAGACGTGACACCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC	1081
Db	961	GGAGCAGACGTGACACCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC	1020
QY	1082	TTTTCAAAAGGATCCTTTTCATATAGAGAACACACTGAGAGATACTTGAAGAAATTTGGATT	1141
Db	1021	TTTTCAAAAGGATCCTTTTCATATAGAGAACACACTGAGAGATACTTGAAGAAATTTGGATT	1080
QY	1142	CAGCCCGCAGAGATTTTATCAGCTTAACCTCAGATATAATCATTTGAAGTAATAGGTAAA	1201
Db	1081	CAGCCCGCAGAGATTTTATCAGCTTAACCTCAGATATAATCATTTGAAGTAATAGGTAAA	1140
QY	1202	AGCTAGTCTTCACTTCCAGGGCCGACGGCTCAGAGTAATTTGAATAGCATTTTACAGTG	1261
Db	1141	AGCTAGTCTTCACTTCCAGGGCCGACGGCTCAGAGTAATTTGAATAGCATTTTACAGTG	1200
QY	1262	TAGAGTAAACATTAACATTTGATATGATGAGAAACATGAGAGAACATATTACAGTGTCTTA	1321
Db	1201	TAGAGTAAACATTAACATTTGATATGATGAGAAACATGAGAGAACATATTACAGTGTCTTA	1260
QY	1322	CCACTCTATATCAAGAAAAGAAATTACAGACTCTGATTTCTACAGTGTATGATTAATCTTAAA	1381
Db	1261	CCACTCTATATCAAGAAAAGAAATTACAGACTCTGATTTCTACAGTGTATGATTAATCTTAAA	1320
QY	1382	AATGTTATTCATATAGGGCTTTTGATTTATAAACCCTTGGTACTATATCTAAATATATGT	1441
Db	1321	AATGTTATTCATATAGGGCTTTTGATTTATAAACCCTTGGTACTATATCTAAATATATGT	1380
QY	1442	AGTTATTTGCTTCCAGTTTGCTTGATATATTTTGTGATTTAAGATTCTTGACTTATA	1501
Db	1381	AGTTATTTGCTTCCAGTTTGCTTGATATATTTTGTGATTTAAGATTCTTGACTTATA	1440
QY	1502	TTTTTAATGGGTTCTAGTGAAGAAAAGAAATGATATATTTCTGTAAGACATCGATATACATTT	1561
Db	1441	TTTTTAATGGGTTCTAGTGAAGAAAAGAAATGATATATTTCTGTAAGACATCGATATACATTT	1500
QY	1562	ATTTACACTCTTGATTTCTACAAATGTAGAAAATGAGAGAAATGCCACAAATTTGATGTGAT	1621
Db	1501	ATTTACACTCTTGATTTCTACAAATGTAGAAAATGAGAGAAATGCCACAAATTTGATGTGAT	1560
QY	1622	AAAAGTCAAGTGAACAGA 1640	
Db	1561	AAAAGTCAAGTGAACAGA 1579	
RESULT 11			
US-09-030-606-107			
: Sequence 107. Application US/09030606			
: Patent No. US20020081580A1			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F			
: NUMBER OF SEQUENCES: 224			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: SEED AND BERRY LLP			
: STREET: 6300 Columbia Center, 701 Fifth Avenue			
: CITY: Seattle			
: STATE: WA			
: COUNTRY: USA			
: ZIP: 98104			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			

```

? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA: US/09/030,606
? FILING DATE: 25-FEB-1998
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: MAKI, David J.
? REGISTRATION NUMBER: 31,392
? TELECOMMUNICATION DOCKET NUMBER: 210121.428C3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 622-4900
? TELEFAX: (206) 682-6031
? INFORMATION FOR SEQ ID NO: 107:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1621 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
?
US-09-030-606-107

Query Match          78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      62  GCCCATGGACATGCAAGGGCATCTGGGTGTGAAGTCGTCGGCCCGTGGCCCCGGGCCGTT 121
        |||||||
DB       1  GCCCATGGACATGCAAGGGCATCTGGGTCAATGAGCTGTCCGGCTTGCCCCGGGCCGTT 60
        |||||||

QY      122 CTGTCTATGTGTCACGCGTCACTTCGGGGCGCGTGTGTACGCCTGGACCGCGGCCGCTC 181
        |||||||
DB       61 CTGTCTATGTGTCACGCGTCACTTCGGGGCGCGTGTGTACGCCTGGACCGCGGCCGCTC 120
        |||||||

QY      182 CCGCTACACACGTGACCCCGTTGGCCCGGGACAAGCGCTCGTAAGTCGTCGACTCAAGA 241
        |||||||
DB       121 CGGCTACACACGTGACCCCGTTGGCCCGGGACAAGCGCTCGTAAGTCGTCGACTCAAGA 180
        |||||||

QY      242 GCAGGGGAGACCGCGGTCGCGGCGTGTGCAAGCGGTCGATGTGTCTGCTGGAGCC 301
        |||||||
DB       181 GCAGGGGAGACCGCGGTCGCGGCGTGTGCAAGCGGTCGATGTGTCTGCTGGAGCC 240
        |||||||

QY      302 CTTCGCGCGCGGTGTGATGAGAACTCGACGTGGGCCCAAGATTTCTGACCGGGAAAA 361
        |||||||
DB       241 CTTCGCGCGCGGTGTGATGAGAACTCGACGTGGGCCCAAGATTTCTGACCGGGAAAA 300
        |||||||

QY      362 TCCAAGGCTATTATTTATGCCAGGCTGAGTGATTTGGCAGTCAGGAACCTTCGCCGTT 421
        |||||||
DB       301 TCCAAGGCTATTATTTATGCCAGGCTGAGTGATTTGGCAGTCAGGAACCTTCGCCGTT 360
        |||||||

QY      422 AGCTGGCCACGATATCAACTATTGGCTTTGTACAGTGTTCTCTCAAAAATTTGSCAAG 481
        |||||||
DB       361 AGCTGGCCACGATATCAACTATTGGCTTTGTACAGTGTTCTCTCAAAAATTTGSCAAG 420
        |||||||

QY      482 TGCTGAGATTCGTTATGCCCGCGCTAAATTCCTGGCTGACTTGTGGGGGTGGCCTAT 541
        |||||||
DB       421 TGCTGAGATTCGTTATGCCCGCGCTAAATTCCTGGCTGACTTGTGGGGGTGGCCTAT 480
        |||||||

QY      542 GTGTCACTGGGCAATTATATGCTCTTTTTGACCACACGACACTGGCAAGGTCAGGT 601
        |||||||
DB       481 GTGTCACTGGGCAATTATATGCTCTTTTTGACCACACGACACTGGCAAGGTCAGGT 540
        |||||||

QY      602 CATTCATCAAAATATGTGTGAAGAACAACATATTTAAAGTCTTTTCTGTGTGAAAAC 661
        |||||||
DB       541 CATTCATCAAAATATGTGTGAAGAACAACATATTTAAAGTCTTTTCTGTGTGAAAAC 600
        |||||||

QY      662 GAATTCGAGTCTGTGTGGGAAGACCTCTCGAGGACAGAAACATGTGGATGTGGGGAGCACCTTT 721
        |||||||
DB       601 GAATTCGAGTCTGTGTGGGAAGACCTCTCGAGGACAGAAACATGTGGATGTGGGGAGCACCTTT 660
        |||||||

QY      722 CATTCAGCACTTACAGACAGCAGATGGGGAAATTCATGTGCTGTTGGAGCAATGAACCCCA 781
        |||||||

```



```

Db 661 CTAATACGACTTACAGAGACAGATGGGGAAATTCATGGCTGTGGAGCAATAGAACCCCA 720
Qy 782 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGTAGAACTTCCCAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGTAGAACTTCCCAATCAGAT 780
Qy 842 GAGCATGATGATGGCCAGAAATGAAAGAAAGATTGGCAGATGATTTGGCAAGAGAC 901
Db 781 GAGCATGATGATGGCCAGAAATGAAAGAAAGATTGGCAGATGATTTGGCAAGAGAC 840
Qy 902 GAAGGAGAGAGTGTGTAATCTTTGAGGAGCAAGATGGCTGTGATCCGCTTGCAG 961
Db 841 GAAGGAGAGTGTGTAATCTTTGAGGAGCAAGATGGCTGTGATCCGCTTGCAG 900
Qy 962 TTTTGAAGAGTGTGCTCATGATCAACAAAGAGAGGGGCTGTGTTATCACCAGTA 1021
Db 901 TTTTGAAGAGTGTGCTCATGATCAACAAAGAGAGGGGCTGTGTTATCACCAGTA 960
Qy 1022 GGAGCAGACGTGAGCCCGCCCTGCACTGTGTTAAACCCAGCCATCCCTTC 1081
Db 961 GGAGCAGACGTGAGCCCGCCCTGCACTGTGTTAAACCCAGCCATCCCTTC 1020
Qy 1082 TTTTCAAAAGGATCTTTCATAGAGAAACACAGTGAAGATCTTGAAGATTTGGATT 1141
Db 1021 TTTTCAAAAGGATCTTTCATAGAGAAACACAGTGAAGATCTTGAAGATTTGGATT 1080
Qy 1142 CAGCCGCGAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAGTAATAAGTAAA 1201
Db 1081 CAGCCGCGAGAGATTTATCAGCTTAACCTAGATAAAATCATTTGAAGTAATAAGTAAA 1140
Qy 1202 AGCTAGTCTTAATCTTCAGGCGCCAGGCTCAAGTGAATTTGAATACGTATTAACAGTG 1261
Db 1141 AGCTAGTCTTAATCTTCAGGCGCCAGGCTCAAGTGAATTTGAATACGTATTAACAGTG 1200
Qy 1262 TAGAGTAACACATTAATGATGATGAGAAACATGAGAGAACTATTAAGTGTCTTA 1321
Db 1201 TAGAGTAACACATTAATGATGATGAGAAACATGAGAGAACTATTAAGTGTCTTA 1260
Qy 1322 CCACCTTAATCAAGAAAGATTCAGACTGTGATTCACAGTGAATTAATTCATAA 1381
Db 1261 CCACCTTAATCAAGAAAGATTCAGACTGTGATTCACAGTGAATTAATTCATAA 1320
Qy 1382 AATGTTATCATTAAGGCTTTGATTTATTAACCTTGGGTACTTATTAATTAATGAT 1441
Db 1321 AATGTTATCATTAAGGCTTTGATTTATTAACCTTGGGTACTTATTAATTAATGAT 1380
Qy 1442 AGTTATTCGCTTCAGATTTGCTGATATATTTGATATTAAGATTTCTTGACTATA 1501
Db 1381 AGTTATTCGCTTCAGATTTGCTGATATATTTGATATTAAGATTTCTTGACTATA 1440
Qy 1502 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTTGAAGCATCGATATACATTT 1561
Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTTGAAGCATCGATATACATTT 1500
Qy 1562 AATTACACCTGATTCACAAATGTAGAAATGAGAAATGCGCAAAATTTGATGGAT 1621
Db 1501 AATTACACCTGATTCACAAATGTAGAAATGAGAAATGCGCAAAATTTGATGGAT 1560
Qy 1622 AAAAGTCACGTGAACAGA 1640
Db 1561 AAAAGTCACGTGAACAAA 1579

```

```

; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-107

Query Match      78.5%  Score 1574.2  DB 10:  Length 1621;
Best Local Similarity 99.8%  Pred No. 0:
Matches 1576;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0:

Qy 62 CGCATGAGACGTCAGAGGACATTTGGCTGCTGAGAGCTGTCCGGCTGCGCCGGCCGCTT 121
Db 1 CGCATGAGACGTCAGAGGACATTTGGCTGCTGAGAGCTGTCCGGCTGCGCCGGCCGCTT 60
Qy 122 CTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
Db 61 CTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 182 CCGCTACGACGTGAGCCCGCTTGGGCGCGGCAAGCGCTGCTAGTGTGAGCTGAAGCA 241
Db 121 CCGCTACGACGTGAGCCCGCTTGGGCGCGGCAAGCGCTGCTAGTGTGAGCTGAAGCA 180
Qy 242 GCGCGGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
Db 181 GCGCGGCGGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 302 CTTCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 241 CTTCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 362 TCCAGAGCTTATTTATGTCAGAGCTGATGATTTGGCCAGTGAAGAACTTCTGCGGCTT 421
Db 301 TCCAGAGCTTATTTATGTCAGAGCTGATGATTTGGCCAGTGAAGAACTTCTGCGGCTT 360
Qy 422 AGCTGGCCAGATATCACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAG 481
Db 361 AGCTGGCCAGATATCACTATTTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAG 420
Qy 482 TGGTGAAGATCCGTATGCGCCGCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 541
Db 421 TGGTGAAGATCCGTATGCGCCGCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 480
Qy 542 GTGTGCACTGGGCAATTAATAGGCTTTTGTGACCGCACACGACGCTGCAAGGGTCAAGT 601
Db 481 GTGTGCACTGGGCAATTAATAGGCTTTTGTGACCGCACACGACGCTGCAAGGGTCAAGT 540
Qy 602 CATTTGATGCAAAATATGCGGAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAGATCA 661
Db 541 CATTTGATGCAAAATATGCGGAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAGATCA 600
Qy 662 GAATGAGACTGTGTGGAGAGACCTCGAGGACAGAACATGTTGATGGTGGAGAGACCTTT 721
Db 601 GAATGAGACTGTGTGGAGAGACCTCGAGGACAGAACATGTTGATGGTGGAGAGACCTTT 660
Qy 722 CTATACGACTTACAGACAGCAGATGCGGGAATTCATAGCTGTTGAGCAATAGAACCCCA 781
Db 661 CTATACGACTTACAGACAGCAGATGCGGGAATTCATAGCTGTTGAGCAATAGAACCCCA 720
Qy 782 GTTCTACGAGCTGCTGATCAAAAGAGACTTGAAGTGTGATGAAGTCTCCAAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAAAGAGACTTGAAGTGTGATGAAGTCTCCAAATCAGAT 780
Qy 842 GAGCATGATGATGGCCAGAAATGAAAGAAAGATTGGCAGATGATTTGGCAAGAGAC 901
Db 781 GAGCATGATGATGGCCAGAAATGAAAGAAAGATTGGCAGATGATTTGGCAAGAGAC 840
Qy 902 GAAGGAGAGTGTGTAATCTTTGAGGAGCAAGATGGCTGTGATCCGCTTGCAG 961
Db 841 GAAGGAGAGTGTGTAATCTTTGAGGAGCAAGATGGCTGTGATCCGCTTGCAG 900

```

```

RESULT 12
US-09-822-827-107
; Sequence 107, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827

```

QY 962 TTTTGGAGAGTTGTCATCATGATCACAACAAGGAGGCGCTTATATCAGAGTGA 1021
|||||
Db 901 TTTTGGAGAGTTGTCATCATGATCACAACAAGGAGGCGCTTATATCAGAGTGA 960
QY 1022 GGAGCAGAGCTGAGGCCCCCGCTGACCTGCTGCTTTAAACACCCGACCATCCCTTC 1081
|||||
Db 961 GGAGCAGAGCTGAGGCCCCCGCTGACCTGCTGCTTTAAACACCCGACCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTTCATAGAGAACACACTGAGGAGATCTTGAAGAATTTGGATT 1141
|||||
Db 1021 TTTCAAAAGGATCTTTTCATAGAGAACACACTGAGGAGATCTTGAAGAATTTGGATT 1080
QY 1142 CAGCCCGGAGAGATTTATCAGCTTACCTGATGATTAATCATTTGAAAGTAAAGSTAAA 1201
|||||
Db 1081 CAGCCCGGAGAGATTTATCAGCTTACCTGATGATTAATCATTTGAAAGTAAAGSTAAA 1140
QY 1202 AGCTAGTCTTACCTTCCAGGCGCCAGGCGCTCAAGTGAATTTGAATTCGTATTCAGAGTG 1261
|||||
Db 1141 AGCTAGTCTTACCTTCCAGGCGCCAGGCGCTCAAGTGAATTTGAATTCGTATTCAGAGTG 1200
QY 1262 TAGAGTACACATTAACATTTGATGATGAGAACATGAGAGAACATTAATTCAGTGTCTTA 1321
|||||
Db 1201 TAGAGTACACATTAACATTTGATGATGAGAACATGAGAGAACATTAATTCAGTGTCTTA 1260
QY 1322 CCAGCTTATCAAGAAAAGATTTACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1381
|||||
Db 1261 CCAGCTTATCAAGAAAAGATTTACAGACTCTGATTTCTACAGTGAATTTGAAATTTCTAAA 1320
QY 1382 AATGTTATCATTAAGGCGCTTTTGTATTAATTTGTTGATTAATTAAGATTTCTGACTTATA 1441
|||||
Db 1321 AATGTTATCATTAAGGCGCTTTTGTATTAATTTGTTGATTAATTAAGATTTCTGACTTATA 1380
QY 1442 AGTTATTTGCTTCCAGTTTGGCTGTATATATTTGTTGATTAATTAAGATTTCTGACTTATA 1501
|||||
Db 1381 AGTTATTTGCTTCCAGTTTGGCTGTATATATTTGTTGATTAATTAAGATTTCTGACTTATA 1440
QY 1502 TTTTGAATGGGTTCTGATGAAAAAGAAATGATATATTTCTTGAAGACATGATTAATTTT 1561
|||||
Db 1441 TTTTGAATGGGTTCTGATGAAAAAGAAATGATATATTTCTTGAAGACATGATTAATTTT 1500
QY 1562 ATTACACTCTTGATTTCTACATATGTAAGAAATGAGAAATGCCAAATTTGATGGTAT 1621
|||||
Db 1501 ATTACACTCTTGATTTCTACATATGTAAGAAATGAGAAATGCCAAATTTGATGGTAT 1560
QY 1622 AAAAGTCAGCTGAACAGA 1640
|||||
Db 1561 AAAAGTCAGCTGAACAAA 1579
RESULT 13
US-09-115-453-107
; Sequence 107, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-107
Query Match 78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGACAGGCGCATCTCGGTCTGAGCTGTCCCGGCTGGCCCCCGGCGCTT 121
Db 1 CGCCATGGCACTGACAGGCGCATCTCGGTCTGAGCTGTCCCGGCTGGCCCCCGGCGCTT 60
QY 122 CTGTGCTATGCTCTGGCTGACTTCCGGGCGCCTGTGAGTAAAGCTGTGACCGCGCGGCTC 181
|||||
Db 61 CTGTGCTATGCTCTGGCTGACTTCCGGGCGCCTGTGAGTAAAGCTGTGACCGCGCGGCTC 120
QY 182 CCGCTACGAGCTGAGGCGCGCTGAGGCGGCAAGCGCTGCTAGTCTGTGACCTGGAAGA 241
|||||
Db 121 CCGCTACGAGCTGAGGCGCGCTGAGGCGGCAAGCGCTGCTAGTCTGTGACCTGGAAGA 180
QY 242 GCCGCGGAGAGCCCGGCTGCTGCTGTCTGTCAAGCGGTCGAGATGCTGTGACGCC 301
|||||
Db 181 GCCGCGGAGAGCCCGGCTGCTGCTGTCTGTCAAGCGGTCGAGATGCTGTGACGCC 240
QY 302 CTTCGCGCGGCGGCTATGAGAGAACTCCAGCTGGGCGCAAGATCTGAGCGGGGAAAA 361
|||||
Db 241 CTTCGCGCGGCGGCTATGAGAGAACTCCAGCTGGGCGCAAGATCTGAGCGGGGAAAA 300
QY 362 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGAAAGCTTTCGCCGTT 421
|||||
Db 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGAAAGCTTTCGCCGTT 360
QY 422 AGCTGCGCACGATATCACTATTTGGCTTTGTAGAGTGTCTCTCAAAAATTTGGCAGAG 481
|||||
Db 361 AGCTGCGCACGATATCACTATTTGGCTTTGTAGAGTGTCTCTCAAAAATTTGGCAGAG 420
QY 482 TGGTGAAGATCCGTATGCGCGCGCTGAATCTCGTGGTGAATTTGCTGAGTGGGCTTAT 541
|||||
Db 421 TGGTGAAGATCCGTATGCGCGCGCTGAATCTCGTGGTGAATTTGCTGAGTGGGCTTAT 480
QY 542 GTGTGACATGGGCAATTAATATGCTCTTTTGAACCGCACAGCAGTGGCAAGGCTCAGGT 601
|||||
Db 481 GTGTGACATGGGCAATTAATATGCTCTTTTGAACCGCACAGCAGTGGCAAGGCTCAGGT 540
QY 602 CATTGATGCAAAATATGCTGGAAGAGAACAGCATTTTAAGTCTCTTTCTGTGAAAACTTA 661
|||||
Db 541 CATTGATGCAAAATATGCTGGAAGAGAACAGCATTTTAAGTCTCTTTCTGTGAAAACTTA 600
QY 662 GAATGAGAGCTGTGGGAAAGCACCTCGAGGACAGAACATGTTGAGTGTGAGCACCTTT 721
|||||
Db 601 GAATGAGAGCTGTGGGAAAGCACCTCGAGGACAGAACATGTTGAGTGTGAGCACCTTT 660
QY 722 CTATACGACTTACAGCAGACAGATGGGAAATTCATGCTGTTGAGCAATAGAACCCCA 781
|||||
Db 661 CTATACGACTTACAGCAGACAGATGGGAAATTCATGCTGTTGAGCAATAGAACCCCA 720
QY 782 GTTCTAGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 841
|||||
Db 721 GTTCTAGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAATCCCAATCAGAT 780
QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGATTTTGAAGAAGAGC 901
|||||
Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGATTTTGAAGAAGAGC 840
QY 902 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTTCTGAC 961
|||||
Db 841 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTTCTGAC 900
QY 962 TTTTGGAGAGGTTGTCATCATGATCACAACAAGAGGCGGCTGTTATACACAGTGA 1021
|||||
Db 901 TTTTGGAGAGGTTGTCATCATGATCACAACAAGAGGCGGCTGTTATACACAGTGA 960
QY 1022 GGAGCAGAGCTGAGGCCCCCGCTGACCTGCTGCTTAAACACCCGACCATCCCTTC 1081
|||||
Db 961 GGAGCAGAGCTGAGGCCCCCGCTGACCTGCTGCTTAAACACCCGACCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTTCATAGAGAACACACTGAGAGATCTTGAAGAATTTGGATT 1141
|||||
Db 1021 TTTCAAAAGGATCTTTTCATAGAGAACACACTGAGAGATCTTGAAGAATTTGGATT 1080
QY 1142 CAGCCCGGAGAGATTTATCAGCTTACCTGATGATTAATCATTTGAAAGTAAAGSTAAA 1201

```
|||||
Db 1081 CAGCCGCGAGAGATTTATCAGTTAACTCAGATTAATAATGATTAAGTAAAGTAA 1140
QY 1202 AGCTAGCTCTTAAGCTTCAGGCGCCAGGCTCAAGTAATTTGAATTCGATTTACAGTG 1261
Db 1141 AGCTAGCTCTTAAGCTTCAGGCGCCAGGCTCAAGTAATTTGAATTCGATTTACAGTG 1200
QY 1262 TAGAGTAACATTAACATTTATGATGATGAAACATGAGAGAACAGTATTTACAGTGCTCA 1321
Db 1201 TAGAGTAACATTAACATTTATGATGATGAAACATGAGAGAACATGATTTACAGTGCTCA 1260
QY 1322 CCAGCTTAATCAGAAAGATTTACAGACTCTGATTTCTACAGTATGATGATTAATTTAA 1381
Db 1261 CCAGCTTAATCAGAAAGATTTACAGACTCTGATTTCTACAGTATGATGATTAATTTAA 1320
QY 1382 AATGGTATCATAGGAGGCTTTGATTTATTAACCTTTGGGCTCTTATCTAAATTAATGAT 1441
Db 1321 AATGGTATCATAGGAGGCTTTGATTTATTAACCTTTGGGCTCTTATCTAAATTAATGAT 1380
QY 1442 AGTTATTCGCTTCAGATTTGCTTGATATTTGTTGATATTAAGATTTCTTGACCTTATA 1501
Db 1381 AGTTATTCGCTTCAGATTTGCTTGATATTTGTTGATATTAAGATTTCTTGACCTTATA 1440
QY 1502 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATTTCTTGAAGACATGATATACATTT 1561
Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATTTCTTGAAGACATGATATACATTT 1500
QY 1562 ATTTACACTCTGATTTCTACATGTAGAAATGAGAAATGCCACAATTTGATATGATAT 1621
Db 1501 ATTTACACTCTGATTTCTACATGTAGAAATGAGAAATGCCACAATTTGATATGATAT 1560
QY 1622 AAAAGTCAGGTGAACAGA 1640
Db 1561 AAAAGTCAGGTGAACAGA 1579

RESULT 14
US-09-967-305-6
; Sequence 6, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLAQUA-COA RACEMASE IN HORMONE
; FILE REFERENCE: 0734-312001
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 3654
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(1271)
US-09-967-305-6

Query Match 59.78; Score 1197; DB 10; Length 3654;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 121 TCTGTGCTATGAGTCTCTGCTGATCTTGGGGCGCTGTGAGTACGCTGAGCCGCGCT 180
Db 145 TCTGTGCTATGAGTCTCTGCTGATCTTGGGGCGCTGTGAGTACGCTGAGCCGCGCT 204
QY 181 CCGGCTACAGCAGTGAAGCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGAGACTGAAAG 240
Db 205 CCGGCTACAGCAGTGAAGCGCTTTGGGCGGGGCAAGCGCTCGCTAGTGTGAGACTGAAAG 264
QY 241 AGCGGCGGGAGCCCGCTGTGCTGCGGCTGTGCAAGCGGCTGAGTGTGCTGTGAGAG 300
Db 265 AGCGGCGGGAGCCCGCTGTGCTGCGGCTGTGCAAGCGGCTGAGTGTGCTGTGAGAG 324
QY 301 CCGTCCGCGCGGCTGTGCAAGGAACTCCAGCTGCGGCGCCAGAGATTTGCAAGCGGCA 360
Db 325 CCGTCCGCGCGGCTGTGCAAGGAACTCCAGCTGCGGCGCCAGAGATTTGCAAGCGGCA 384
QY 361 ATCCAAAGCTTATTTATGCGCAGGCTGATGATTTGGCCAGTCAAGAAAGCTTTCGCGGT 420
Db 385 ATCCAAAGCTTATTTATGCGCAGGCTGATGATTTGGCCAGTCAAGAAAGCTTTCGCGGT 444
QY 421 TAGCTGGCCAGCATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAA 480
Db 445 TAGCTGGCCAGCATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAA 504
QY 481 GTGCTGAGAAATCCGATATCCCGCTGAATCTCTGCGCTGACTTCTGCTGTGCGCTTA 540
Db 505 GTGCTGAGAAATCCGATATCCCGCTGAATCTCTGCGCTGACTTCTGCTGTGCGCTTA 564
QY 541 TGTGTGCTATGGGCAATTTAATGAGCTCTTTTGAACCGCAGCAGCACTGGCAAGGCTCAG 600
Db 565 TGTGTGCTATGGGCAATTTAATGAGCTCTTTTGAACCGCAGCAGCACTGGCAAGGCTCAG 624
QY 601 TCAATGATGCAAAATATGCTGGAAGAAACAGCAATTAATTAATTTCTTCTGTGGAAGATC 660
Db 625 TCAATGATGCAAAATATGCTGGAAGAAACAGCAATTAATTAATTTCTTCTGTGGAAGATC 684
QY 661 AGAATCGAGTCTGTGGGAGACACCTTGAGGACAGCAACTGTTGATGTGTGAGACACTT 720
Db 685 AGAATCGAGTCTGTGGGAGACACCTTGAGGAGCAAGCAATGTTGATGTGTGAGACACTT 744
QY 721 TCTATGAGCTTACAGGACAGCAGATGGGGAATTCATGAGCTTTGAGCAATTAAGACCCC 780
Db 745 TCTATGAGCTTACAGGACAGCAGATGGGGAATTCATGAGCTTTGAGCAATTAAGACCCC 804
QY 781 AGTTCTACAGCTGCTGATCAAAAGACTTGAAGTGTGATGATGATGATGATGATGATGAT 840
Db 805 AGTTCTACAGCTGCTGATCAAAAGACTTGAAGTGTGATGATGATGATGATGATGATGAT 864
QY 841 TGAGCATGATATGGCCAGAAATGAAGAAAGTGTGACAGATGATATTTGCAAGAGAGA 900
Db 865 TGAGCATGATATGGCCAGAAATGAAGAAAGTGTGACAGATGATATTTGCAAGAGAGA 924
QY 901 CGAAGCAGAGTGTGCAAAATCTTTGAGGCGCAGATGCTGTGATGCTCGGTTCTGA 960
Db 925 CGAAGCAGAGTGTGCAAAATCTTTGAGGCGCAGATGCTGTGATGCTCGGTTCTGA 984
QY 961 CTTTGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 985 CTTTGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1044
QY 1021 AGGAGCAGAGCTGAGCCCGCTGACCTGCTGCTGTTAAACACCCCAAGCTTCTT 1080
Db 1045 AGGAGCAGAGCTGAGCCCGCTGACCTGCTGCTGTTAAACACCCCAAGCTTCTT 1104
QY 1081 CTTTCAAAAAGGATCTTTTCAATAGAGAACACACTGAGAGATTTGATGAAATTTGAT 1140
Db 1105 CTTTCAAAAAGGATCTTTTCAATAGAGAACACACTGAGAGATTTGATGAAATTTGAT 1164
QY 1141 TCAGCCGCGAAGAGATTTATGAGCTTAATCAAGATTAATTAATTAATTAATTAATTA 1197
Db 1165 TCAGCCGCGAAGAGATTTATGAGCTTAATCAAGATTAATTAATTAATTAATTAATTA 1221
```

```

RESULT 15
US-09-967-305-3
; Sequence 3, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1146)
US-09-967-305-3

```

```

Query Match          57.2%; Score 1146; DB 10; Length 1146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 66 ATGGCACTGCGAGGCGATCTGCTGCTGAGAGCTGTCGCGGCTGCGGCGGCGGCTGCTG 125
   |||||||
DB 1 ATGGCACTGCGAGGCGATCTGCTGCTGAGAGCTGTCGCGGCTGCGGCGGCGGCTGCTG 60
QY 126 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 185
   |||||||
DB 61 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 186 TACGAGCTGAGCGGCTTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245
   |||||||
DB 121 TACGAGCTGAGCGGCTTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 246 CGGGGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305
   |||||||
DB 181 CGGGGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 306 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 365
   |||||||
DB 241 CGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 366 AGGCTATTATTATCCAGAGCTGAGTGGATTTGGCCAGTCAAGAAAGCTTCTCCGGTTAGCT 425
   |||||||
DB 301 AGGCTATTATTATCCAGAGCTGAGTGGATTTGGCCAGTCAAGAAAGCTTCTCCGGTTAGCT 360
QY 426 GGCACAGATATCAACTATTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
   |||||||
DB 361 GGCACAGATATCAACTATTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 486 GAGAAATCCGATATCCCGGCTGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
   |||||||
DB 421 GAGAAATCCGATATCCCGGCTGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 546 GCACCTGGCATTTAATGGCTCTTTTGGACCGACAGACGCTGGCAAGGGTCAAGTCAAT 605
   |||||||
DB 481 GCACCTGGCATTTAATGGCTCTTTTGGACCGACAGACGCTGGCAAGGGTCAAGTCAAT 540
QY 606 GATGCAAAATATGCTGGAAGGAGCAAGCATATTTAGTCTTTCTGCTGGAAGAACTCAAGAA 665
   |||||||
DB 541 GATGCAAAATATGCTGGAAGGAGCAAGCATATTTAGTCTTTCTGCTGGAAGAACTCAAGAA 600
QY 666 TCGAGTCTGTGGAGACACCTCGAGAGACAGAAATGTTGGATGCTGAGACACCTTCTAT 725
   |||||||
DB 601 TCGAGTCTGTGGAGACACCTCGAGAGACAGAAATGTTGGATGCTGAGACACCTTCTAT 660

```

```

QY 726 ACCACTTTACAGACAGACAGATGGGGAAATTCATGCTGTTGGACCAATAGACCCCACTTC 785
   |||||||
DB 661 ACCACTTTACAGACAGACAGATGGGGAAATTCATGCTGTTGGACCAATAGACCCCACTTC 720
QY 786 TACGAGCTGCTGATCAAGAGACTTGGACTAAAGTGGATGATGATGATGATGATGATGATGATG 845
   |||||||
DB 721 TACGAGCTGCTGATCAAGAGACTTGGACTAAAGTGGATGATGATGATGATGATGATGATGATG 780
QY 846 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 905
   |||||||
DB 781 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 906 GCAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGCTGCTGCTGCTGCTGCTGCT 965
   |||||||
DB 841 GCAGAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGCTGCTGCTGCTGCTGCTGCT 900
QY 966 GAGAGAGTGTGTCAATCATGATCATCAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1025
   |||||||
DB 901 GAGAGAGTGTGTCAATCATGATCATCAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 1026 CAGGAGGTGAGCCCGCCCGCCCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1085
   |||||||
DB 961 CAGGAGGTGAGCCCGCCCGCCCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1086 AAAAGGATCTCTTCAATAGAGAGACACACTGAGAGATGATGATGATGATGATGATGATGATG 1145
   |||||||
DB 1021 AAAAGGATCTCTTCAATAGAGAGACACACTGAGAGATGATGATGATGATGATGATGATGATG 1080
QY 1146 CGCGAAGAGATTTATCAGCTTAAGTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1205
   |||||||
DB 1081 CGCGAAGAGATTTATCAGCTTAAGTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1140
QY 1206 AGTCTC 1211
   |||||||
DB 1141 AGTCTC 1146

```

Search completed: April 2, 2003, 02:29:58
Job time : 193.983 secs

OY	122	CTGGCTATGGTCCCTGGGCTACACTTCGGGGCGCGTGGTACGCTGGACCGGGCCGGCGTC	181
Db	61	CTTGCTATGGTCTCTGGCTACCTTCGGGGCGCGTGGTACGCTGGACCGGGCCGGCGTC	120
OY	182	CCGCTACGACCTGAGCCGCTTGGGGCGGGGCAAGCCCTCGCTAGTGCCTGGACCTTAGCA	241
Db	121	CCGCTACGACCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTTAGCA	180
OY	242	GGCCGGGGGACCCCGCTGGTGGCGGCTCTGTGCAAAGCGGTGGAGTGTCTCTGTGAGCC	301
Db	181	GGCCGGGGGACCCCGCTGGTGGCGGCTCTGTGCAAAGCGGTGGAGTGTCTCTGTGAGCC	240
OY	302	CTTCCGCGCGGTCATGTGAGAAACCTCCAGCTGGGGCCCGAGAGATTCTCAGCGGGAAAA	361
Db	241	CTTCCGCGCGGTCATGTGAGAAACCTCCAGCTGGGGCCCGAGAGATTCTCAGCGGGAAAA	300
OY	362	TCCAAGGCTTATTTATGCGACAGCGCTGAGTGGATTGGCCACTGAGAGACTTTCGCCGTT	421
Db	301	TCCAAGGCTTATTTATGCGACAGCGCTGAGTGGATTGGCCACTGAGAGAGCTTTCGCCGTT	360
OY	422	AGCTGGCCACGATATATCAACTATTGGCTTGTCAAGTGTCTCTCAAAATTTGGCAGAG	481
Db	361	AGCTGGCCACGATATATCAACTATTGGCTTGTCAAGTGTCTCTCAAAATTTGGCAGAG	420
OY	482	TGTGTAGATATCCGATGCCCCCGCTGAATCTCTGCGTGACTTGTGCTGTGTGCGCTTAT	541
Db	421	TGTGTAGATATCCGATGCCCCCGCTGAATCTCTGCGTGACTTGTGCTGTGTGCGCTTAT	480
OY	542	GTTGGCACTGGGCTTATTAATGGCTCTTTTGGACCCACACAGCACTGGGCAAGGTCAGT	601
Db	481	GTTGGCACTGGGCTTATTAATGGCTCTTTTGGACCCACACAGCACTGGGCAAGGTCAGT	540
OY	602	CATTGATGCAAAATATGCTGGAGAGAACAGCATATTTAAGTCTTTCTGTGGAAAACTCA	661
Db	541	CATTGATGCAAAATATGCTGGAGAGAACAGCATATTTAAGTCTTTCTGTGGAAAACTCA	600
OY	662	GAAATCGAGTGTGGGAAGACCTCGAGGACAGAACTGGTAGAGTGGTGGAGCACTTT	721
Db	601	GAAATCGAGTGTGGGAAGACCTCGAGGAGCACTCGAGGAGCAAACTGGTAGAGTGGTGGAGCACTTT	660
OY	722	CTATATGCACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	781
Db	661	CTATATGCACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720
OY	782	GTTCTACGAGCTGTGTATCCAAAGGACTGTGACTAAAGTGTATGAACTCCCAATCAAT	841
Db	721	GTTCTACGAGCTGTGTATCCAAAGGACTGTGACTAAAGTGTATGAACTCCCAATCAAT	780
OY	842	GAGCATGGATGATGGCCACAGAAATGGAAGAAAGTTTGCAGATGTAATTTGCCAAAGAAC	901
Db	781	GAGCATGGATGATGGCCACAGAAATGGAAGAAAGTTTGCAGATGTAATTTGCCAAAGAAC	840
OY	902	GAAAGCAGATGGTGTAAATCTTTTGAACGGACACAGATGCTGTGTACTCCGGTTCTGAC	961
Db	841	GAAAGCAGATGGTGTAAATCTTTTGAACGGACACAGATGCTGTGTACTCCGGTTCTGAC	900
OY	962	TTTTGAGAGAGTTTTCATCATGATGATCAACAAGAAAGGAGGCGTGGTTATACACAGGA	1021
Db	901	TTTTGAGAGAGTTTTCATCATGATGATCAACAAGAAAGGAGGCGTGGTTATACACAGGA	960
OY	1022	GGAGCAGAGCTGAGCCCGCCCGCTCAGCTCTGCTTTAAACACCCAGCCATCCCTTC	1081
Db	961	GGAGCAGAGCTGAGCCCGCCCGCTCAGCTCTGCTTTAAACACCCAGCCATCCCTTC	1020
OY	1082	TTTTCAAAAGGATCTTTTCATAGGAGACACACTGAGAGATACTTGAAGAAATTTGGATT	1141
Db	1021	TTTTCAAAAGGATCTTTTCATAGGAGACACACTGAGAGATACTTGAAGAAATTTGGATT	1080
OY	1142	CAGCCGGAAGATTTATAGCTTTAACTCAAGTAAATATCATTTGAGAAATTAAGCTAAA	1201
Db	1081	CAGCCGGAAGATTTATAGCTTTAACTCAAGTAAATATCATTTGAGAAATTAAGCTAAA	1140

QY	1202	AGAGAGCTCAACTTCAGAGCCACAGGGCTCAAGTGAATTTGAAATACGCAATTTCAGTG	1261
Db	1141	AGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAAATACGCAATTTCAGTG	1200
QY	1262	TAGAGTAACACATACATTGTATGCATGTGAACATGGAGGAACAGTATTACAGTGCCTA	1321
Db	1201	TAGAGTAACACATACATTGTATGCATGTGAACATGGAGGAACAGTATTACAGTGCCTA	1260
QY	1322	CCACTCTATACAGAAAAAGAAATTACAGACTCTGATCTCTACAGTGAATGTAATCTAAA	1381
Db	1261	CCACTCTATACAGAAAAAGAAATTACAGACTCTGATCTCTACAGTGAATGTAATCTAAA	1320
QY	1382	AATGGTATCATTTAGGGCTTTTGATTATTAATTAACCTTTGGGTACTATACATAAATTATG	1441
Db	1321	AATGGTATCATTTAGGGCTTTTGATTATTAATTAACCTTTGGGTACTATACATAAATTATG	1380
QY	1442	AGTATATTCGCTTCACAGTTTGCTGTATATATTTGTGATATTAAAGATTTCTGACTATTA	1501
Db	1381	AGTATATTCGCTTCACAGTTTGCTGTATATATTTGTGATATTAAAGATTTCTGACTATTA	1440
QY	1502	TTTGAATAGGGTTCTACGTGAAGAAAGATATATATTTCTTGAAGACATCGATATACATT	1561
Db	1441	TTTGAATAGGGTTCTACGTGAAGAAAGATATATATTTCTTGAAGACATCGATATACATT	1500
QY	1562	ATTTACACTCTTGATTCTACATATGAGAAATGAGAGAAATGCCACAATTTGATGGTAT	1621
Db	1501	ATTTACACTCTTGATTCTACATATGAGAAATGAGAGAAATGCCACAATTTGATGGTAT	1560
QY	1622	AAAAGTCACGTGAACAGA 1640	
Db	1561	AAAAGTCACGTGAACAGA 1579	

RESULT 2
US-09-030-607-107

; Sequence 107, Application US/09030607
; Patent No. 6262245

GENERAL INFORMATION:
APPLICANT: Xu, Ji
APPLICANT: Dillon

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
 NUMBER OF SEQUENCES: 224

;;
;;
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
c/o 3300 G-1 Building
701 F-6th Avenue

STATE: WA
CITY: Seattle
SIREL: 0500

COUNTRY: USA
ZIP: 98104

```

;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compat+ibj10

```

```

; COMPIER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607

```

ATTORNEY/AGENT INFORMATION:
/ CLASSIFICATION:
/ FILING DATE: 25-FEB-1998
/

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR ID NO. 107

```

; INFORMATION FOR SEQ ID NO: 10//
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1621 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
;

```

```
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGIN: SOURCE
```

```

; ORGANISM: Homo sapiens
US-09-030-607-107

Query Match      78.5%; Score 1574.2; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CCCATGCGACTGCGAGGCGATCTGCGTCTGCGAGCTGCTCCGCGCTGGCCCCCGCCGTT 121
    |||||||
DB 1 CCGCATGCGACTGCGAGGCGATCTGCGTCTGCGAGCTGCTCCGCGCTGGCCCCCGCCGTT 60

QY 122 CTGTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
    |||||||
DB 61 CTGTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 182 CCGCTACAGCTGAGCGGCTTGGGCGGCGGCGAAGCGCTGCTAGTGTGAGTCTGAGTGA 241
    |||||||
DB 121 CCGCTACAGCTGAGCGGCTTGGGCGGCGGCGAAGCGCTGCTAGTGTGAGTCTGAGTGA 180

QY 242 GCGCGGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
    |||||||
DB 181 GCGCGGCGGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 302 CTTCGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
    |||||||
DB 241 CTTCGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 362 TCCAGGCTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
    |||||||
DB 301 TCCAGGCTTATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 422 ACCTGCGCAGCATATCAAACTATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
    |||||||
DB 361 ACCTGCGCAGCATATCAAACTATTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 482 TGGTAGAATACCTGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
    |||||||
DB 421 TGGTAGAATACCTGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

QY 542 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
    |||||||
DB 481 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 602 CATTTGATCAAAATATGCTGCGAGGAAACAGCATATTTAAGTCTTTTCTGTGAGAAACTCA 661
    |||||||
DB 541 CATTTGATCAAAATATGCTGCGAGGAAACAGCATATTTAAGTCTTTTCTGTGAGAAACTCA 600

QY 662 GAAATCGAGTCTGTGCGAGACACCTCGAGAGACAGAACTGTTGGATGCTGAGACACTTT 721
    |||||||
DB 601 GAAATCGAGTCTGTGCGAGACACCTCGAGAGACAGAACTGTTGGATGCTGAGACACTTT 660

QY 722 CTATACGACTTACAGAGACAGACAGATGGGAATTCATGCTGTTGAGACATTAAGACCCA 781
    |||||||
DB 661 CTATACGACTTACAGAGACAGACAGATGGGAATTCATGCTGTTGAGACATTAAGACCCA 720

QY 782 GTTCTACAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGACTTCCCAATGAGAT 841
    |||||||
DB 721 GTTCTACAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGACTTCCCAATGAGAT 780

QY 842 GAGCATGATGATGCGCAGAAATGAAGAAATGTTGCAATGATATTTGCAAGAAAGAC 901
    |||||||
DB 781 GAGCATGATGATGCGCAGAAATGAAGAAATGTTGCAATGATATTTGCAAGAAAGAC 840

QY 902 GAAGCAGAGTGTGTCAAATCTTTAGCGGACAGATGCTGTGTGACTCCGGTCTGAC 961
    |||||||
DB 841 GAAGCAGAGTGTGTCAAATCTTTAGCGGACAGATGCTGTGTGACTCCGGTCTGAC 900

QY 962 TTTTGAAGAGGTTGTGATCATGATGACAAAGAGAACGGGGCTGTTTATCAACAGTGA 1021
    |||||||
DB 901 TTTTGAAGAGGTTGTGATCATGATGACAAAGAGAACGGGGCTGTTTATCAACAGTGA 960

QY 1022 GGAGCAGAGCTGAGCCCGCGCTGCTGCTGCTGTTAAACACCCAGCAGCATCCCTTC 1081
    |||||||

```

```

DB 961 GGAGCAGAGCTGAGACCCCGCCGCTGACCTGCTGTTAAACACCCAGCAGCATCCCTTC 1020

QY 1082 TTTCAAAAGGATCTTTTCATAGAGAACACACTGAGAGATCTGGAAGATTTGGATT 1141
    |||||||
DB 1021 TTTTCAAAAGGATCTTTTCATAGAGAACACACTGAGAGATCTGGAAGATTTGGATT 1080

QY 1142 CAGCGCGAGAGATTTATACAGTTAATCAAGATTAATCAATTTGAAAGTAAAGSTAAA 1201
    |||||||
DB 1081 CAGCGCGAGAGATTTATACAGTTAATCAAGATTAATCAATTTGAAAGTAAAGSTAAA 1140

QY 1202 AGCTATGCTTAACTTCACAGGCGCAGGCTCAAGTGAATTTGAATTAAGTATTAAGTGA 1261
    |||||||
DB 1141 AGCTATGCTTAACTTCACAGGCGCAGGCTCAAGTGAATTTGAATTAAGTATTAAGTGA 1200

QY 1262 TAGAGTACATATACATTTGATGATGAGAAACATGAGAGAACATTTACAGTCCCTA 1321
    |||||||
DB 1201 TAGAGTACATATACATTTGATGATGAGAAACATGAGAGAACATTTACAGTCCCTA 1260

QY 1322 CCACTTAATCAGAAAGAAATTAACAGACTGATTTACAGTATGATTTGAATTTCTAAA 1381
    |||||||
DB 1261 CCACTTAATCAGAAAGAAATTAACAGACTGATTTACAGTATGATTTGAATTTCTAAA 1320

QY 1382 AATGCTTATCAATTTAGGCTTTGATTTATAAAACCTTTGGTACTTATACATAATATGCT 1441
    |||||||
DB 1321 AATGCTTATCAATTTAGGCTTTGATTTATAAAACCTTTGGTACTTATACATAATATGCT 1380

QY 1442 AGTTATTCGCTTCCAGTTTGGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1501
    |||||||
DB 1381 AGTTATTCGCTTCCAGTTTGGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1440

QY 1502 TTTTGAATGAGGTTCTAGTGAAGAAAGAAATGATATTTCTGSAAGACATGATTTACATT 1561
    |||||||
DB 1441 TTTTGAATGAGGTTCTAGTGAAGAAAGAAATGATATTTCTGSAAGACATGATTTACATT 1500

QY 1562 ATTTACACTCTGTTGCTCAATGATGAGAAAGAAAGCCCAAAATGATGCTGAT 1621
    |||||||
DB 1501 ATTTACACTCTGTTGCTCAATGATGAGAAAGAAAGCCCAAAATGATGCTGAT 1560

QY 1622 AAAAGTACGTAAGAACGA 1640
    |||||||
DB 1561 AAAAGTACGTAAGAACGA 1579

RESULT 3
US-09-605-785-107
; Sequence 107, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Shagan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolky, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605.785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107

```

LENGTH: 1621
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-605-785-107

Query Match 78.5%; Score 1574.2; DB 4; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 62 CGCATGACATGACAGGATCTGGTCTGAGAGCTGCGCGCTGAGCCCGGCGCTT 121
DB 1 CGCATGACATGACAGGATCTGGTCTGAGAGCTGCGCGCTGAGCCCGGCGCTT 60
QY 122 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
DB 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 182 CGGCTACGAGCTGAGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 241
DB 121 CGGCTACGAGCTGAGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 180
QY 242 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 301
DB 181 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 240
QY 302 CTTCGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
DB 241 CTTCGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 362 TCCAGAGCTTATTTATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
DB 301 TCCAGAGCTTATTTATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 422 AGCTGCGCAGATATCACTATTTGGCTTGTGAGGTGTCTCTCAAAAATTTGGCAGAG 481
DB 361 AGCTGCGCAGATATCACTATTTGGCTTGTGAGGTGTCTCTCAAAAATTTGGCAGAG 420
QY 482 TGTGTGAATCCGTATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
DB 421 TGTGTGAATCCGTATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 542 GTGTGACTGGGCTATTTATGCTTGTGAGCGGCGGCGGCGGCGGCGGCT 601
DB 481 GTGTGACTGGGCTATTTATGCTTGTGAGCGGCGGCGGCGGCGGCGGCT 540
QY 602 CATGTATGCAAAATATGTTGGAAGAACAGCATATTTAAGTCTTTCTGTGGAATCTCA 661
DB 541 CATGTATGCAAAATATGTTGGAAGAACAGCATATTTAAGTCTTTCTGTGGAATCTCA 600
QY 662 GAAATGGAATCTGTGGGAAGCACTGAGAGCAAGAACATGTTGGATGTGGAGCCTTT 721
DB 601 GAAATGGAATCTGTGGGAAGCACTGAGAGCAAGAACATGTTGGATGTGGAGCCTTT 660
QY 722 CTATACGACTTACAGAGCAGAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 781
DB 661 CTATACGACTTACAGAGCAGAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAAAGCACTTGAATGATGATGATGATGATGATGAT 841
DB 721 GTTCTACGAGCTGCTGATCAAAAGCACTTGAATGATGATGATGATGATGATGAT 780
QY 842 GAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 901
DB 781 GAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 902 GAAGGAGAGTGTGCTCAATCTTTGAGGCGCAGATGCTGTGTGCTGCTGCTGCTGAC 961
DB 841 GAAGGAGAGTGTGCTCAATCTTTGAGGCGCAGATGCTGTGTGCTGCTGCTGCTGAC 900
QY 962 TTTTGAAGAGTGTGCTCATCATGATCACAAGAGAGGCGCTGCTTATCATCCAGTGA 1021
DB 901 TTTTGAAGAGTGTGCTCATCATGATCACAAGAGAGGCGCTGCTTATCATCCAGTGA 960

```

```

QY 1022 GGAGCAGAGCTGAGCCCGCCCGCTGACCTGCTGCTTAAACCCCAACCCATCCCTTC 1081
DB 961 GGAGCAGAGCTGAGCCCGCCCGCTGACCTGCTGCTTAAACCCCAACCCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTATAGAGAACACACTGAGGATGATGATGATGATGATGAT 1141
DB 1021 TTTCAAAAGGATCTTTATAGAGAACACACTGAGGATGATGATGATGATGATGAT 1080
QY 1142 CAGCCGCGAAGATTTATCAGCTTAACCTGATGATGATGATGATGATGATGATGAT 1201
DB 1081 CAGCCGCGAAGATTTATCAGCTTAACCTGATGATGATGATGATGATGATGATGAT 1140
QY 1202 AGCTAGCTCTTAATCTTCAAGCCCGCAGGCTCAAGTAAATTTGATGATGATGAT 1261
DB 1141 AGCTAGCTCTTAATCTTCAAGCCCGCAGGCTCAAGTAAATTTGATGATGATGAT 1200
QY 1262 TAGAGTACATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
DB 1201 TAGAGTACATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1322 CCACCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTATGATGATGATGAT 1381
DB 1261 CCACCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTATGATGATGATGAT 1320
QY 1382 AATGTTATCATAGGCGCTTTGATTTATTAACCTTGGGTACTTATTAATTTATGAT 1441
DB 1321 AATGTTATCATAGGCGCTTTGATTTATTAACCTTGGGTACTTATTAATTTATGAT 1380
QY 1442 AGTTATTTGCTGCTTCCAGTTTGTGATGATGATGATGATGATGATGATGATGAT 1501
DB 1381 AGTTATTTGCTTCCAGTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1502 TTTTGAATGGTCTAGTGAAGAAAGATGATATTTTGAAGATGATGATGATGAT 1561
DB 1441 TTTTGAATGGTCTAGTGAAGAAAGATGATATTTTGAAGATGATGATGATGAT 1500
QY 1562 ATTTACACTCTGATCTCAATGATGAAATGAGAAATGCAACAAATTTGATGATGAT 1621
DB 1501 ATTTACACTCTGATCTCAATGATGAAATGAGAAATGCAACAAATTTGATGATGAT 1560
QY 1622 AAAAGTCACTGAAACAGA 1640
DB 1561 AAAAGTCACTGAAACAGA 1579

```

```

RESULT 4
US-09-439-313-107
; Sequence 107, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuxui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-107

```


Query Match 78.5%; Score 1574.2; DB 4; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 GCGCATGCGACTGAGAGGCGATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGCCGTT 121
 |||||||
 Db 1 CCGCATGCGACTGAGAGGCGATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGCCGTT 60

QY 122 CTGTCTATGCTGCTGCTGCTACTTCCGGGCGGCTGTGGTAGCCGTGAGCCGGCCGCTC 181
 |||||||
 Db 61 CTGTCTATGCTGCTGCTGCTACTTCCGGGCGGCTGTGGTAGCCGTGAGCCGGCCGCTC 120

QY 182 CCGCTACACGTGAGAGCGCTTGGGCGGAGGCGCTCGCTAGTGGCGGAGCTGAAAGA 241
 |||||||
 Db 121 CCGCTACACGTGAGAGCGCTTGGGCGGAGGCGCTCGCTAGTGGCGGAGCTGAAAGA 180

QY 242 GCGGCGGAGAGCGCGCGTGTGGGGGCTGTGCAAGGCGTGGATGCTGCTGGAGAGC 301
 |||||||
 Db 181 GCGGCGGAGAGCGCGCGTGTGGGGGCTGTGCAAGGCGTGGATGCTGCTGGAGAGC 240

QY 302 CTTCGCGCGCGGCTGCTCATGAGAACTCCAGCTGGGCGGAGATTCGACGCGGAGAA 361
 |||||||
 Db 241 CTTCGCGCGCGGCTGCTCATGAGAACTCCAGCTGGGCGGAGATTCGACGCGGAGAA 300

QY 362 TCCAAAGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTACAGGAAGCTTTCGCGGTT 421
 |||||||
 Db 301 TCCAAAGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTACAGGAAGCTTTCGCGGTT 360

QY 422 AGCTGGCCAGCATATCAACTATTTGGCTTTGTAGGCTTCTCTCAAAAATTTGGCAGAG 481
 |||||||
 Db 361 AGCTGGCCAGCATATCAACTATTTGGCTTTGTAGGCTTCTCTCAAAAATTTGGCAGAG 420

QY 482 TGGTGAAGATCCGATATGCCCCGCTGATCTCGTGGCTACTTTCGTGATGCGCTTAT 541
 |||||||
 Db 421 TGGTGAAGATCCGATATGCCCCGCTGATCTCGTGGCTACTTTCGTGATGCGCTTAT 480

QY 542 GTGTGACATGGGCAATTAATGAGCTCTTTTGGCGGCAAGCACTGGCAAGGCTACAGT 601
 |||||||
 Db 481 GTGTGACATGGGCAATTAATGAGCTCTTTTGGCGGCAAGCACTGGCAAGGCTACAGT 540

QY 602 CATGTATGCAAAATATGTTGGAGGAAGCAACATATTTAAGTCTTTCTGTCGGAAGATCA 661
 |||||||
 Db 541 CATGTATGCAAAATATGTTGGAGGAAGCAACATATTTAAGTCTTTCTGTCGGAAGATCA 600

QY 662 GAAATCGAGTCTGTGGAGACCTCGAGGACAGAACTGTTGGATGGTGAGACCTTT 721
 |||||||
 Db 601 GAAATCGAGTCTGTGGAGACCTCGAGGACAGAACTGTTGGATGGTGAGACCTTT 660

QY 722 CTATACGACTTACAGAGACAGACAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 781
 |||||||
 Db 661 CTATACGACTTACAGAGACAGACAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720

QY 782 GTTCTACGAGTCTGTGATCAAAAGACTTGAAGTCTGATGAGCTTCCCAATCAGAT 841
 |||||||
 Db 721 GTTCTACGAGTCTGTGATCAAAAGACTTGAAGTCTGATGAGCTTCCCAATCAGAT 780

QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAAAGATTTGAGATGATTTTGAAGAAAGAC 901
 |||||||
 Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAAGATTTGAGATGATTTTGAAGAAAGAC 840

QY 902 GAAGGCAAGTGTGCTCAAAATCTTTGAGGCGACAGATGCTGTGAGCTCGGTTCTGAC 961
 |||||||
 Db 841 GAAGGCAAGTGTGCTCAAAATCTTTGAGGCGACAGATGCTGTGAGCTCGGTTCTGAC 900

QY 962 TTTTGAAGAGTGTCTCATCATCATGATCAACAAGAGAGAGGCGCTGTTTATCACAGTGA 1021
 |||||||
 Db 901 TTTTGAAGAGTGTCTCATCATCATGATCAACAAGAGAGAGGCGCTGTTTATCACAGTGA 960

QY 1022 GGAGCAGAGAGTGAAGCCCGCCCTGACCTGCTGCTTTTAAACACCCAGCAATCCCTTC 1081
 |||||||
 Db 961 GGAGCAGAGAGTGAAGCCCGCCCTGACCTGCTGCTTTTAAACACCCAGCAATCCCTTC 1020

QY 1082 TTTCAAAAGGATCTCTTTCATAGAGAGACACACTGAGAGATCTTGAAGATTTGGATT 1141
 |||||||
 Db 1021 TTTCAAAAGGATCTCTTTCATAGAGAGACACACTGAGAGATCTTGAAGATTTGGATT 1080

QY 1142 CAGCGCGCAAGATTTATTCAGCTTAACCTACAGATTAATCAATTTGAAGATTAAGGTAA 1201
 |||||||
 Db 1081 CAGCGCGCAAGATTTATTCAGCTTAACCTACAGATTAATCAATTTGAAGATTAAGGTAA 1140

QY 1202 AGCTAGTCTTAATCTTCAGAGGCGCAAGGCTCAAGTGAATTTGAATAGATTTACAGTG 1261
 |||||||
 Db 1141 AGCTAGTCTTAATCTTCAGAGGCGCAAGGCTCAAGTGAATTTGAATAGATTTACAGTG 1200

QY 1262 TAGAGTACACATATACATTTGTATGATGAGAAACATGAGAGACATTTACAGTCTCTA 1321
 |||||||
 Db 1201 TAGAGTACACATATACATTTGTATGATGAGAAACATGAGAGACATTTACAGTCTCTA 1260

QY 1322 CCACCTATATCAAGAAAGAAATTTACAGACTGATCTTACAGTATGATTTGAATTTCTAA 1381
 |||||||
 Db 1261 CCACCTATATCAAGAAAGAAATTTACAGACTGATCTTACAGTATGATTTGAATTTCTAA 1320

QY 1382 AATGCTATATCAATTTAGGCGCTTTGATTTAAACTTTGGTACTTATTAATTTATGCT 1441
 |||||||
 Db 1321 AATGCTATATCAATTTAGGCGCTTTGATTTAAACTTTGGTACTTATTAATTTATGCT 1380

QY 1442 AGTTATTCGCTTCCAGTTTGGCTGATATATTTGTTGATATTTAAGATTTCTGACTTATA 1501
 |||||||
 Db 1381 AGTTATTCGCTTCCAGTTTGGCTGATATATTTGTTGATATTTAAGATTTCTGACTTATA 1440

QY 1502 TTTTGAATGAGGTTCTAGTAAAGAAATGATATATTTCTTGAAGACATCATATACATT 1561
 |||||||
 Db 1441 TTTTGAATGAGGTTCTAGTAAAGAAATGATATATTTCTTGAAGACATCATATACATT 1500

QY 1562 ATTTACACTCTTGAATGATGTAAGAAATGAGAAATGCCCAAAATTTGATGATGAT 1621
 |||||||
 Db 1501 ATTTACACTCTTGAATGATGTAAGAAATGAGAAATGCCCAAAATTTGATGATGAT 1560

QY 1622 AAAAGTCAGTGAACAGA 1640
 |||||||
 Db 1561 AAAAGTCAGTGAACAAA 1579

RESULT 5
 US-09-352-616A-107
 ; Sequence 107; Application US/09352616A
 ; Patent No. 6395278
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillion, Davin C.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang, Yuqi
 ; APPLICANT: Xu, Jlangchun
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.427C8
 ; CURRENT APPLICATION NUMBER: US/09/352,616A
 ; CURRENT FILING DATE: 1999-07-13
 ; NUMBER OF SEQ ID NOS: 472
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 107
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-352-616A-107

Query Match 78.5%; Score 1574.2; DB 4; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CCGCATGCGACTGAGAGGCGATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGCCGTT 121
 |||||||
 Db 1 CCGCATGCGACTGAGAGGCGATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGCCGTT 60

QY 122 CTGTCTATGCTGCTGCTGCTACTTCCGGGCGGCTGTGGTAGCCGTGAGCCGGCCGCTC 181
 |||||||
 Db 61 CTGTCTATGCTGCTGCTGCTACTTCCGGGCGGCTGTGGTAGCCGTGAGCCGGCCGCTC 120

QY 182 CCGCTACACGTGAGAGCGCTTGGGCGGAGGCGCTCGCTAGTGGCGGAGCTGAAAGA 241
 |||||||
 Db 121 CCGCTACACGTGAGAGCGCTTGGGCGGAGGCGCTCGCTAGTGGCGGAGCTGAAAGA 180

QY 242 GCGGCGGAGAGCGCGCGTGTGGGGGCTGTGCAAGGCGTGGATGCTGCTGGAGAGC 301
 |||||||
 Db 181 GCGGCGGAGAGCGCGCGTGTGGGGGCTGTGCAAGGCGTGGATGCTGCTGGAGAGC 240

QY 302 CTTCGCGCGCGGCTGCTCATGAGAACTCCAGCTGGGCGGAGATTCGACGCGGAGAA 361
 |||||||
 Db 241 CTTCGCGCGCGGCTGCTCATGAGAACTCCAGCTGGGCGGAGATTCGACGCGGAGAA 300

QY 362 TCCAAAGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTACAGGAAGCTTTCGCGGTT 421
 |||||||
 Db 301 TCCAAAGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTACAGGAAGCTTTCGCGGTT 360

QY 422 AGCTGGCCAGCATATCAACTATTTGGCTTTGTAGGCTTCTCTCAAAAATTTGGCAGAG 481
 |||||||
 Db 361 AGCTGGCCAGCATATCAACTATTTGGCTTTGTAGGCTTCTCTCAAAAATTTGGCAGAG 420

QY 482 TGGTGAAGATCCGATATGCCCCGCTGATCTCGTGGCTACTTTCGTGATGCGCTTAT 541
 |||||||
 Db 421 TGGTGAAGATCCGATATGCCCCGCTGATCTCGTGGCTACTTTCGTGATGCGCTTAT 480

QY 542 GTGTGACATGGGCAATTAATGAGCTCTTTTGGCGGCAAGCACTGGCAAGGCTACAGT 601
 |||||||
 Db 481 GTGTGACATGGGCAATTAATGAGCTCTTTTGGCGGCAAGCACTGGCAAGGCTACAGT 540

QY 602 CATGTATGCAAAATATGTTGGAGGAAGCAACATATTTAAGTCTTTCTGTCGGAAGATCA 661
 |||||||
 Db 541 CATGTATGCAAAATATGTTGGAGGAAGCAACATATTTAAGTCTTTCTGTCGGAAGATCA 600

QY 662 GAAATCGAGTCTGTGGAGACCTCGAGGACAGAACTGTTGGATGGTGAGACCTTT 721
 |||||||
 Db 601 GAAATCGAGTCTGTGGAGACCTCGAGGACAGAACTGTTGGATGGTGAGACCTTT 660

QY 722 CTATACGACTTACAGAGACAGACAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 781
 |||||||
 Db 661 CTATACGACTTACAGAGACAGACAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720

QY 782 GTTCTACGAGTCTGTGATCAAAAGACTTGAAGTCTGATGAGCTTCCCAATCAGAT 841
 |||||||
 Db 721 GTTCTACGAGTCTGTGATCAAAAGACTTGAAGTCTGATGAGCTTCCCAATCAGAT 780

QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAAAGATTTGAGATGATTTTGAAGAAAGAC 901
 |||||||
 Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAAGATTTGAGATGATTTTGAAGAAAGAC 840

QY 902 GAAGGCAAGTGTGCTCAAAATCTTTGAGGCGACAGATGCTGTGAGCTCGGTTCTGAC 961
 |||||||
 Db 841 GAAGGCAAGTGTGCTCAAAATCTTTGAGGCGACAGATGCTGTGAGCTCGGTTCTGAC 900

QY 962 TTTTGAAGAGTGTCTCATCATCATGATCAACAAGAGAGAGGCGCTGTTTATCACAGTGA 1021
 |||||||
 Db 901 TTTTGAAGAGTGTCTCATCATCATGATCAACAAGAGAGAGGCGCTGTTTATCACAGTGA 960

QY 1022 GGAGCAGAGAGTGAAGCCCGCCCTGACCTGCTGCTTTTAAACACCCAGCAATCCCTTC 1081
 |||||||
 Db 961 GGAGCAGAGAGTGAAGCCCGCCCTGACCTGCTGCTTTTAAACACCCAGCAATCCCTTC 1020

Db	61	CTGTGCTATGGTCTCTGGCTGACTTCGGGGGGCGGCTGTGTACGGCTGGACCGGCCGGCTTC	120
Qy	182	CCGCTACGACCTGAGCCGCTTGGGCGGGGCAAGCGTCCCTAGTGTGGACTGAAGA	241
Db	121	CCGCTACGACCTGAGCCGCTTGGGCGGGGCAAGCGTCCCTAGTGTGGACTGAAGA	180
Qy	242	GCCGGGGGAGCCCCCGCTGCTGGCGGCTCTGTGTCCAAAGCGGTGGATGTGCTGTGAAGC	301
Db	181	GCCGGGGGAGCCCCCGTGTGGCGGCTCTGTGTCAAGCGGTGGATGTGCTGTGAAGC	240
Qy	302	CTTCCGCCGCGGTCTCATGGAAGAACTCCAGCTGGGCCAGAGATTCCTGCAGCGGGAAAA	361
Db	241	CTTCCGCCGCGGTCTCATGGAAGAACTCCAGCTGGGCCAGAGATTCCTGCAGCGGGAAAA	300
Qy	362	TCCAAGGCTTTTATATGCGAGCGCTGATGGATTTGGCCTACAGAGAAAGCTTCTCGCGGTT	421
Db	301	TCCAAGGCTTTTATATGCGAGCGCTGATGGATTTGGCCTACAGAGAAAGCTTCTCGCGGTT	360
Qy	422	AGCTGGCCACGATATFCAACTATTTGGCTTTGTGATAGTGTCTCTCAAAAATTGGCAGAG	481
Db	361	AGCTGGCCACGATATFCAACTATTTGGCTTTGTGATAGTGTCTCTCAAAAATTGGCAGAG	420
Qy	482	TGTGTGAAATCCGATATGCCCGCGCTGAATCTTCCTGTGCTGACTTTGTGTGTGGCTTAT	541
Db	421	TGTGTGAAATCCGATATGCCCGCGCTGAATCTTCCTGTGCTGACTTTGTGTGTGGCTTAT	480
Qy	542	GTTGTGCACTGGGGCAATTAATAGCGCTCTTTTGTGACCGCACAGCATGGCAGGAGGTAGGT	601
Db	481	GTTGTGCACTGGGGCAATTAATAGCGCTCTTTTGTGACCGCACAGCATGGCAGGAGGTAGGT	540
Qy	602	CATTGATGCAAAATATGTGTGGAAGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCA	661
Db	541	CATTGATGCAAAATATGTGTGGAAGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCA	600
Qy	662	GAAATCGAGTGTGGGAGAGACCTCGAGACAGAACATTTGGAGTGGGAGACACTTT	721
Db	601	GAAATCGAGTGTGGGAGAGACCTCGAGACAGAACATTTGGAGTGGGAGACACTTT	660
Qy	722	CTATACGACTTACAGGACAGCAGATGGGGAAATTCATGCGCTGTTTGAGACAATAGAACCCA	781
Db	661	CTATACGACTTACAGGACAGCAGATGGGGAAATTCATGCGCTGTTTGAGACAATAGAACCCA	720
Qy	782	GTTCTACGAGCTGTGATTCAAAGGACTGTGGACATTAAGTCTGATGAATCCCAATAGAT	841
Db	721	GTTCTACGAGCTGTGATTCAAAGGACTGTGGACATTAAGTCTGATGAATCCCAATAGAT	780
Qy	842	GAGCATGGATATTTGGCCAGAGAAATGAAGAAGATTGGCAGATGTATTTTGCAAAAGAGAC	901
Db	781	GAGCATGGATATTTGGCCAGAGAAATGAAGAAGATTGGCAGATGTATTTTGCAAAAGAGAC	840
Qy	902	GAAAGCAGAGTGTGTGTAATCTTTGACGGCACAGATGCTGTGTGATCTCGGTTTGTAC	961
Db	841	GAAAGCAGAGTGTGTGTAATCTTTGACGGCACAGATGCTGTGTGATCTCGGTTTGTAC	900
Qy	962	TTTTGAGAGAGTGTATATCATATGATGCACACAAGAAAGCGGCGTCTTTATCCACAGTA	1021
Db	901	TTTTGAGAGAGTGTATATCATATGATGCACACAAGAAAGCGGCGTCTTTATCCACAGTA	960
Qy	1022	GGAGCAGAGAGTGTAGCCCCCGCCCTGCACTGTGTGTAAACACCCAGCCATCCCTTC	1081
Db	961	GGAGCAGAGAGTGTAGCCCCCGCCCTGCACTGTGTGTAAACACCCAGCCATCCCTTC	1022
Qy	1082	TTTCAAAAAGGATCTTTCATATAGAGAAACACACTGAGAGATATCTTGAAGAATTTGGATT	1141
Db	1021	TTTCAAAAAGGATCTTTCATATAGAGAAACACACTGAGAGATATCTTGAAGAATTTGGATT	1080
Qy	1142	CAGCCGGGAAGAGATTTATATAGCTTAACTAGATTAATAATCATTAAGAAATTAAGGTAA	1201
Db	1081	CAGCCGGGAAGAGATTTATATAGCTTAACTAGATTAATAATCATTAAGAAATTAAGGTAA	1141
Qy	1202	AGCTAGTCTTAAGTTCACAGGCCCGCGCTCAAGTGAATTTGAATATCTGCATTTACAGTG	1261

Dp	1141	AGTAGCTCTACCTTCAGAGCCACAGGCTCAAGTGAATTTGAAATACGATTTACAGTG	1200
Qy	1262	TAGAGTAAACATPACCTTTGTATGCATGGAACATGAGAACAGATTTACAGTGCTCTA	1321
Dp	1201	TAGAGTAAACATPACATTTGTATGATGGAACATGAGAAACAGATTTACAGTGCTCTA	1260
Qy	1322	CCACTCAATCAAGAAAGAATTAACAGACTCGATTCTCAAGTGTGATTTGAATTTCTAAA	1381
Dp	1261	CCACTCAATCAAGAAAGAATTAACAGACTCGATTCATCACTGATGATTTGAATTTCTAAA	1320
Qy	1382	AATGGTTATCATTAAGGCTTTGTATTTATPAAACTTTGGGTCTATPACTAAATTATGCT	1441
Dp	1321	AATGGTTATCATTAAGGCTTTGTATTTATPAAACTTTGGGTCTATPACTAAATTATGCT	1380
Qy	1442	AGTATTTCTGCTTCCAGTTGGTGTATPATTGTTGATATTAAGATTTCTGACTATPA	1501
Dp	1381	AGTATTTCTGCTTCCAGTTGGTGTATPATTGTTGATATTAAGATTTCTGACTATPA	1440
Qy	1502	TTTTGAATGGGTTCTACGTGAAAAAGAAATGATTTATTTCTTGAAGACATGATATACATTT	1561
Dp	1441	TTTTGAATGGGTTCTACGTGAAAAAGAAATGATTTATTTCTTGAAGACATGATATACATTT	1500
Qy	1562	ATTTTACACTCTTGATTTCTACATGTAGAAAATGAGAAATGCCACAATTTGTATGCTGAT	1621
Dp	1501	ATTTTACACTCTTGATTTCTACATGTAGAAAATGAGAAATGCCACAATTTGTATGCTGAT	1560
Qy	1622	AAAGTCACGTGAAGACA 1640	
Dp	1561	AAAGTCACGTGAAGACA 1579	

```

RESULT 6
US-09-232-149A-107
: Sequence 107, Application US/09232149A
: Patent No. 6465611
: GENERAL INFORMATION:
: APPLICANT: Xu, Jieqinchan
: APPLICANT: Dillon, David C
: APPLICANT: Micham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHER
: FILE REFERENCE: 210121.427C6
: CURRENT APPLICATION NUMBER: US/09/232.149A
: CURRENT FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 338
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 107
: LENGTH: 1621
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-232-149A-107

```

Query Match	78.5%;	Score 1574.2;	DB 4;	Length 1621;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1576;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0;

QY	CGATATGGCACTGGAGGGGCAATCTGGGTCGTGGAGACTCTCCGGCCCTGGCCCGGGCCCGCTT	121
Db	1 CGCCATGGCACTGGAGGGGCAATCTGGTATATGAGACTGTCCGGCTGGCCCGGGCCCGCTT	60
QY	122 CTGTCTATGTCTCTGGCTGACTCTCGGGGGCGCGTGTGTGTACGCGCTGGACCGGGCCGGCTC	181
Db	61 CTGTGTATGTCTCTGGCTGACTCTCGGGGGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	120
QY	182 CCGCTAGACGCTGAGCCGCTTGGGGCGGGGGCAGCGCTCCGTAGTGTCTGGAACTGAAAGCA	241
Db	61 CCGCTAGACGCTGAGCCGCTTGGGGCGGGGGCAGCGCTCCGTAGTGTGTGTGTGTGTGTGTGTGTGT	180
QY	121 CCGCTAGACGCTGAGCCGCTTGGGGCGGGGGCAGCGCTCCGTAGTGTGTGTGTGTGTGTGTGTGTGT	180
Db	121 CCGCTAGACGCTGAGCCGCTTGGGGCGGGGGCAGCGCTCCGTAGTGTGTGTGTGTGTGTGTGTGTGT	180
QY	242 GCCCGGGGAGACCCCGTCGTGCGCGGCGTCGTGTGCAACCGGCGGATGTGTCGTGGAGCC	301
Db	181 GCCCGGGGAGACCCCGTCGTGCGCGGCGTCGTGTGCAACCGGTCGATGTGCTGTGGAGCC	240
QY	302 CTTTCCGCGCGGTGCATGGAGAAATCCAGTCCAGTGGGCCAGAGATTTCGACGCGGGAAAA	361

Page 7

Db	1321	AAAGCTTATCATTCAGCGCTTTTGATTTATTA	AAAACTTGGGACTTATACAAATATATGCT	1380
Oy	1442	AGTATATTCGCTCCGACAGTATTCGTGATAT	ATATTTGTGATATTAAGATTCCTTGACTATA	1501
Db	1381	AGTATATTCGCTCCGACAGTATTCGTGATAT	ATATTTGTGATATTAAGATTCCTTGACTATA	1440
Oy	1502	TTTTGAATGGGTTCTAGTGA	AAAAAGAAATGATATATCTTGAACACTGCATATTT	1561
Db	1441	TTTTGAATGGGTTCTAGTGA	AAAAAGAAATGATATATCTTGAACACTGCATATTT	1500
Oy	1562	ATTTACACTCTTGATTTCTACATGTG	AGAAAATGAGAAATGCCCAATTTGTATGCTGAT	1621
Db	1501	ATTTACACTCTTGATTTCTACATGTG	AGAAAATGAGAAATGCCCAATTTGTATGCTGAT	1560
Oy	1622	AAAACTCAGCTGAACAACA	1640	
Db	1561	AAAACTCAGCTGAACAACA	1579	
RESULT 7				
US-09-020-956-74				
Sequence 74, Application US/09020956				
Patent No. 6261562				
GENERAL INFORMATION:				
APPLICANT: Xu, Jiangchun				
APPLICANT: Dillin, David C.				
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS				
NUMBER OF SEQUENCES: 178				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: SEED and BERRY LLP				
STREET: 6300 Columbia Center, 701 Fifth Avenue				
CITY: Seattle				
STATE: WA USA				
COUNTRY: USA				
ZIP: 98104				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: Patent Release #1.0, Version #1.30				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/09/020,956				
FILING DATE: 09-FEB-1998				
CLASSIFICATION:				
ATTORNEY/AGENT INFORMATION:				
NAME: MAKI, David J.				
REGISTRATION NUMBER: 31,392				
REFERENCE/DOCKET NUMBER: 210121.427C2				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: (206) 622-4900				
TELEFAX: (206) 682-6031				
INFORMATION FOR SEQ ID NO: 74:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 537 base pairs				
TYPE: nucleic acid				
STRANDEDNESS: single				
TOPOLOGY: linear				
MOLECULE TYPE: cDNA				
ORIGINAL SOURCE:				
ORGANISM: Homo sapiens				
US-09-020-956-74				
Query Match				
Best Local Similarity 98.5%; Score 515; DB 4; Length 537;				
Best Local Similarity 98.5%; Pred. No. 3.8e-136;				
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;				
Oy	1097	TTTTCATGAGGAAACACACTGAGAGATTA	CTTGAGAAATTTGCGATTCAGCCGAGAGAGAT	1156
Db	1	TTTTCATGAGGAAACACACTGAGAGATTA	CTTGAGAAATTTGCGATTCAGCCGAGAGAGAT	60
Oy	1157	TTTTCAGCTTAACCTAGATAAATCATTA	TAAGCTAAATTAACCTGTGTCTAACT	1216
Db	61	TTTTCAGCTTAACCTAGATAAATCATTA	TAAGCTAAATTAACCTGTGTCTAACT	120

```

: RESULT 9
: US-09-605-785-74
: Sequence 74, Application US/09605785
: Patent No. 6321716
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuguai
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skelky, Vasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C16
: CURRENT APPLICATION NUMBER: US/09/605,785
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 835.
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 74
: LENGTH: 537
: TYPE: DNA
:

```


OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-74

Query Match 25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1097 TTTTCATAGGAGAACACACTGAGAGATCTTGAAGATTGGATTCAGCCGCGAGAGAT 1156
|||||
Db 1 TTTTCATAGGAGAACACACTGAGAGATCTTGAAGATTGGATTCAGCCGCGAGAGAT 60
QY 1157 TTTTCAGCTTAACCTGATTAATAATCTTGAAGATTGGATTCAGCTTCAACT 1216
|||||
Db 61 TTTTCAGCTTAACCTGATTAATAATCTTGAAGATTGGATTCAGCTTCAACT 120
QY 1217 TCCAGGCCACGCTCAAGTGAATTTGAATTCATTTACAGTGTAGAGTACACATTA 1276
|||||
Db 121 TCCAGGCCACGCTCAAGTGAATTTGAATTCATTTACAGTGTAGAGTACACATTA 180
QY 1277 CATTTGATGATGAGAACATGAGAACAGTATTACAGTGTCTACCACTCTAATCAGA 1336
|||||
Db 181 CATTTGATGATGAGAACATGAGAACAGTATTACAGTGTCTACCACTCTAATCAGA 240
QY 1337 AAGAAATTACAGCTGCTGATTTCTACAGTATGATTAATTTCTAATAATGGTTATCATTTAG 1396
|||||
Db 241 AAGAAATTACAGCTGCTGATTTCTACAGTATGATTAATTTCTAATAATGGTTATCATTTAG 300
QY 1397 GCGTTTGAATTTTAAACCTTTGGTACTTATCTAATTAATGTTATTCGCTTC 1456
|||||
Db 301 GCGTTTGAATTTTAAACCTTTGGTACTTATCTAATTAATGTTATTCGCTTC 360
QY 1457 CAGTTTGCCTTGATATTTTGTGATATTAAGATTCTTGACTATATTTGAATGGTTCT 1516
|||||
Db 361 CAGTTTGCCTTGATATTTTGTGATATTAAGATTCTTGACTATATTTGAATGGTTCT 420
QY 1517 AGTGAAGAAAGATGATATTTCTTGAAGCATGATATCATTTTATACACTCTTGAT 1576
|||||
Db 421 ACTGAAGAAAGATGATATTTCTTGAAGCATGATATCATTTTATACACTCTTGAT 480
QY 1577 TCTACATGTAGAAAATG-AGGAAATGCCACAATTTGTATGATGATTAAGTCCGT 1632
|||||
Db 481 TCTACATGTAGAAAATGAGGAAATGCCCAATTTGTATGATGATTAAGTCCGT 537

RESULT 12

US-09-232-149A-74
; Sequence 74, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(537)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-74

Query Match 25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1097 TTTTCATAGGAGAACACACTGAGAGATCTTGAAGATTGGATTCAGCCGCGAGAGAT 1156
|||||
Db 1 TTTTCATAGGAGAACACACTGAGAGATCTTGAAGATTGGATTCAGCCGCGAGAGAT 60
QY 1157 TTTTCAGCTTAACCTGATTAATAATCTTGAAGATTGGATTCAGCTTCAACT 1216
|||||
Db 61 TTTTCAGCTTAACCTGATTAATAATCTTGAAGATTGGATTCAGCTTCAACT 120
QY 1217 TCCAGGCCACGCTCAAGTGAATTTGAATTCATTTACAGTGTAGAGTACACATTA 1276
|||||
Db 121 TCCAGGCCACGCTCAAGTGAATTTGAATTCATTTACAGTGTAGAGTACACATTA 180
QY 1277 CATTTGATGATGAGAACATGAGAACAGTATTACAGTGTCTACCACTCTAATCAGA 1336
|||||
Db 181 CATTTGATGATGAGAACATGAGAACAGTATTACAGTGTCTACCACTCTAATCAGA 240
QY 1337 AAGAAATTACAGCTGCTGATTTCTACAGTATGATTAATTTCTAATAATGGTTATCATTTAG 1396
|||||
Db 241 AAGAAATTACAGCTGCTGATTTCTACAGTATGATTAATTTCTAATAATGGTTATCATTTAG 300
QY 1397 GCGTTTGAATTTTAAACCTTTGGTACTTATCTAATTAATGTTATTCGCTTC 1456
|||||
Db 301 GCGTTTGAATTTTAAACCTTTGGTACTTATCTAATTAATGTTATTCGCTTC 360
QY 1457 CAGTTTGCCTTGATATTTTGTGATATTAAGATTCTTGACTATATTTGAATGGTTCT 1516
|||||
Db 361 CAGTTTGCCTTGATATTTTGTGATATTAAGATTCTTGACTATATTTGAATGGTTCT 420
QY 1517 AGTGAAGAAAGATGATATTTCTTGAAGCATGATATCATTTTATACACTCTTGAT 1576
|||||
Db 421 ACTGAAGAAAGATGATATTTCTTGAAGCATGATATCATTTTATACACTCTTGAT 480
QY 1577 TCTACATGTAGAAAATG-AGGAAATGCCACAATTTGTATGATGATTAAGTCCGT 1632
|||||
Db 481 TCTACATGTAGAAAATGAGGAAATGCCCAATTTGTATGATGATTAAGTCCGT 537

RESULT 13

US-09-020-956-3/C
; Sequence 3, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-09-020-956-3

Query Match 20.3%; Score 406.6; DB 4; Length 773;
 Best Local Similarity 98.6%; Pred. No. 2,4e-105;
 Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 676 GGGAGACACCTCGAGACAGAACTGTTGGATGTTGAGACACCTTTCTATACGACTTACA 735
 111
 DB 415 GGGCCCCCTCGAGAGAGAACTGTTGGATGTTGAGACACCTTTCTATACGACTTACA 356
 111
 QY 736 GGACAGCAATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 795
 111
 DB 355 GGACAGCAATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 296
 111
 QY 796 TGATCAAGAGACTTGAGCAATGCTGATGAATCTCCCAATCAGATGAGCATGATGATT 855
 111
 DB 295 TGATCAAGAGANNITGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGATGATT 236
 111
 QY 856 GGCCAGAAATGAAGAAGCTTTCAGATGATATTGCAAAAGACGAGCAGAGTGT 915
 111
 DB 235 GGCCAGAAATGAAGAAGCTTTCAGATGATATTGCAAAAGACGAGCAGAGTGT 176
 111
 QY 916 GTCAATCTTTGAGCGCAGACAGTCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTG 975
 111
 DB 175 GTCAATCTTTGAGCGCAGACAGTCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTG 116
 111
 QY 976 TTGATCATGATACAAAGAGACGGGCTGTTTATCACAGTAGAGAGCAGACTGA 1035
 111
 DB 115 TTGATCATGATACAAAGAGACGGGCTGTTTATCACAGTAGAGAGCAGACTGA 56
 111
 QY 1036 GCCCGCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTCAAAAG 1090
 111
 DB 55 GCCCGCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTCAAAAG 1

RESULT 14

US-09-030-607-3/C
 Sequence 3, Application US/09030607
 Patent No. 6262245
 GENERAL INFORMATION:
 APPLICANT: Xu, JIANGCHUN
 APPLICANT: DILLON, David C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/030,607
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MAKI, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 773 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-09-030-607-3

Query Match 20.3%; Score 406.6; DB 4; Length 773;
 Best Local Similarity 98.6%; Pred. No. 2,4e-105;
 Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 676 GGGAGACACCTCGAGAGAGAACTGTTGGATGTTGAGACACCTTTCTATACGACTTACA 735
 111
 DB 415 GGGCCCCCTCGAGAGAGAACTGTTGGATGTTGAGACACCTTTCTATACGACTTACA 356
 111
 QY 736 GGACAGCAATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 795
 111
 DB 355 GGACAGCAATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 296
 111
 QY 796 TGATCAAGAGACTTGAGCAATGCTGATGAATCTCCCAATCAGATGAGCATGATGATT 855
 111
 DB 295 TGATCAAGAGANNITGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGATGATT 236
 111
 QY 856 GGCCAGAAATGAAGAAGCTTTCAGATGATATTGCAAAAGACGAGCAGAGTGT 915
 111
 DB 235 GGCCAGAAATGAAGAAGCTTTCAGATGATATTGCAAAAGACGAGCAGAGTGT 176
 111
 QY 916 GTCAATCTTTGAGCGCAGACAGTCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTG 975
 111
 DB 175 GTCAATCTTTGAGCGCAGACAGTCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTG 116
 111
 QY 976 TTGATCATGATACAAAGAGACGGGCTGTTTATCACAGTAGAGAGCAGACTGA 1035
 111
 DB 115 TTGATCATGATACAAAGAGACGGGCTGTTTATCACAGTAGAGAGCAGACTGA 56
 111
 QY 1036 GCCCGCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTCAAAAG 1090
 111
 DB 55 GCCCGCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTCAAAAG 1

RESULT 15

US-09-605-785-3/C
 Sequence 3, Application US/09605785
 Patent No. 6321716
 GENERAL INFORMATION:
 APPLICANT: Xu, JIANGCHUN
 APPLICANT: DILLON, David C.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/605,785
 FILING DATE: 2000-06-27
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MAKI, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C16
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NOS: 835
 SEQUENCE CHARACTERISTICS:
 LENGTH: 773
 TYPE: DNA
 ORGANSIM: Homo sapien
 FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
us-09-605-785-3

Query Match 20.3%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 2.4e-105;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
QY 676 GGGAGCACCCTCGAGGAGCAACATGTGATGATGAGCACCCTTCTATACACTTACA 735
    ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 415 GGGCCCCCCTCGAGGAGCAACATGTGATGATGAGCACCCTTCTATACACTTACA 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 736 GGAACAGCAGATGGGAAATTCATGGCTGTTGAGCAATAGAACCCAGTTCTACAGCTGC 795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 355 GGAACAGCAGATGGGAAATTCATGGCTGTTGAGCAATAGAACCCAGTTCTACAGCTGC 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 796 TGATCAAGGACTTGAGCTAAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 855
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 295 TGATCAAGGANTGAGCTAAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 856 GGCAGAAATGAGAGAGATTTGCAGATGATTTGCCAAAGAGAGAGAGAGAGAGTGT 915
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 235 GGCAGAAATGAGAGAGATTTGCAGATGATTTGCCAAAGAGAGAGAGAGAGAGTGT 176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 916 GTCAAAATCTTTGAGGACAGATGCTGTGTGACTCCGGTTCTGACTTTTGAGGAGTTG 975
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 175 GTCAAAATCTTTGAGGACAGATGCTGTGTGACTCCGGTTCTGACTTTTGAGGAGTTG 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 976 TTCATCATGATCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 1035
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 115 TTCATCATGATCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1036 GCCCGCCCTCGACCTGCTGTGTAACACCCAGCAGCATCCCTCTTTCAAAAG 1090
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 55 GCCCGCCCTCGACCTGCTGTGTAACACCCAGCAGCATCCCTCTTTCAAAAG 1
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: April 2, 2003, 02:24:55
Job time : 89.9924 secs

QY 1801 ATGAGAAATGTTGGCTACTAGTAGATCCAGAGGACAGTCACTTTTACGGTTGC 1860
 DB 1801 ATGAGAAATGTTGGCTACTAGTAGATCCAGAGGACAGTCACTTTTACGGTTGC 1860
 QY 1861 CTGTATCCAGTAACATCGGGGCTGTTCCCGGTGCTCTGGCTGTCAGCTTCCCTT 1920
 DB 1861 CTGTATCCAGTAACATCGGGGCTGTTCCCGGTGCTCTGGCTGTCAGCTTCCCTT 1920
 QY 1921 CTGCATGTGTTGATTTCTCTCAGGCTGAGTACAGAGTTCTGATCTTATACCAACACA 1980
 DB 1921 CTGCATGTGTTGATTTCTCTCAGGCTGAGTACAGAGTTCTGATCTTATACCAACACA 1980
 QY 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
 DB 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
 RESULT 2
 AAD38607
 ID AAD38607 standard; cDNA: 2005 BP.
 AC AAD38607;
 DT 23-SEP-2002 (first entry)
 DE Human alpha-methylacyl-CoA racemase splice variant, SV4 cDNA.
 KM Human: prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
 KW cytosolic; SV4; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 66..1214
 FT /tag= a
 FT /product= "Human SV4 protein"
 PN WC200227324-A2.
 PD 04-APR-2002.
 PF 28-SEP-2001; 2001WO-US30532.
 PR 28-SEP-2000; 2000US-236238P.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Richardson J, Monahan J;
 XX WPI: 2002-405070/43.
 DR P-PDB: AAE23975.
 XX Determining risk for prostate cancer in subject or risk for metastatic
 PT prostate cancer to liver or lymph nodes of prostate cancer patients,
 PT racemase measuring expression or activity of alpha-methylacyl-CoA
 PT racemase
 PS Claim 54; Fig 9; 102pp; English.
 CC The present invention relates to novel methods for determining whether
 CC an individual is at risk for prostate cancer or whether a prostate cancer
 CC patient is at risk for metastatic prostate cancer to the liver or lymph
 CC nodes. The method involves measuring the expression or activity of
 CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
 CC in diagnostic methods, drug screening assays, and in treating or
 CC preventing cancer, e.g., prostate cancer. The present sequence is human
 CC alpha-methyl-acyl-CoA racemase splice variant, SV4 cDNA.
 XX Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 other;
 Query Match 99.9%; Score 2003.4; DB 24; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTGACAGGCTGCTGGGCTGAGGCTTAAGGCTGCTCAAGTTTCTTCAGCGGAGCATGAGAA 60
 DB 1 TTGACAGGCTGCTGGGCTGAGGCTTAAGGCTGCTCAAGTTTCTTCAGCGGAGCATGAGAA 60
 QY 61 GGGCCATGGACATCGAGGCAATCTCGTGTGAGACTGTCGGGCTGGCCCGGCGCT 120
 DB 61 GGGCCATGGACATCGAGGCAATCTCGTGTGAGACTGTCGGGCTGGCCCGGCGCT 120
 QY 121 TCTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 121 TCTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 181 CCGCTAGACAGTGAAGCCGCTTGGGCGGAGGCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 CCGCTAGACAGTGAAGCCGCTTGGGCGGAGGCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 AGCGCGGGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 AGCGCGGGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 CCTTCCGCGCGGTGCTCATGAGAAATCCAGTGGGCCAGAGATTCTGACGGGAAA 360
 DB 301 CCTTCCGCGCGGTGCTCATGAGAAATCCAGTGGGCCAGAGATTCTGACGGGAAA 360
 QY 361 ATCCAAAGGCTTATTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAACTTTCGCGGT 420
 DB 361 ATCCAAAGGCTTATTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAACTTTCGCGGT 420
 QY 421 TAGCTGGCCAGATATCAACTATTGGCTTGTGACAGTGTCTCTCAAAATTTGGCAGAA 480
 DB 421 TAGCTGGCCAGATATCAACTATTGGCTTGTGACAGTGTCTCTCAAAATTTGGCAGAA 480
 QY 481 GGGGAGAGATCCGTAATGCCCCGCTGAATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 481 GGGGAGAGATCCGTAATGCCCCGCTGAATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 541 TGTGTGCT 600
 DB 541 TGTGTGCT 600
 QY 601 TCAATTGATGCAATATGCTGAGAGAAACAGATATTTAAAGTTCTTGTGAGAAATCTC 660
 DB 601 TCAATTGATGCAATATGCTGAGAGAAACAGATATTTAAAGTTCTTGTGAGAAATCTC 660
 QY 661 AGAATCGAGTCTGTGGAGAACACCTCGAGAGCAAGAACTGTTGATGTTGAGACACCTT 720
 DB 661 AGAATCGAGTCTGTGGAGAACACCTCGAGAGCAAGAACTGTTGATGTTGAGACACCTT 720
 QY 721 TCTATCGACTTACAGACAGACAGATGGGAATTCATGGCTGTTGAGCAATAGAACCCC 780
 DB 721 TCTATCGACTTACAGACAGACAGATGGGAATTCATGGCTGTTGAGCAATAGAACCCC 780
 QY 781 AGTTCTAGAGCTGTGATCAAGAGACTTGACTAAAGTCTGATGACTGCTGCTGCTGCTGCTGCTGCT 840
 DB 781 AGTTCTAGAGCTGTGATCAAGAGACTTGACTAAAGTCTGATGACTGCTGCTGCTGCTGCTGCTGCT 840
 QY 841 TGAGCATGATGATGGCCAGAAATGAAGAAAGTTGCAAGATGATTTGCAAAAGAA 900
 DB 841 TGAGCATGATGATGGCCAGAAATGAAGAAAGTTGCAAGATGATTTGCAAAAGAA 900
 QY 901 CGAAGCAGAGTGTGTCAAATCTTTGACGCGACAGATGCTGTGTAGCTCCGGTTCTGA 960
 DB 901 CGAAGCAGAGTGTGTCAAATCTTTGACGCGACAGATGCTGTGTAGCTCCGGTTCTGA 960
 QY 961 CTTTGGAGAGTGTTCATCATGATCATCAACAGAGAGAGGAGGCTCTTTATGACCAAGT 1020
 DB 961 CTTTGGAGAGTGTTCATCATGATCATCAACAGAGAGAGGAGGCTCTTTATGACCAAGT 1020
 QY 1021 AGGACGAGAGCTGAGCCCGGCGCTGACACTCTGCTGTTAAACACCCAGCCATCCCTT 1080
 DB 1021 AGGACGAGAGCTGAGCCCGGCGCTGACACTCTGCTGTTAAACACCCAGCCATCCCTT 1080

```

QY 1081 CTTTCAAAAGGATCCTTTCATAGAGAACACACACTGAGAGATCTTGAAGAAATTGGAT 1140
DB 1081 CTTTCAAAAGGATCCTTTCATAGAGAACACACACTGAGAGATCTTGAAGAAATTGGAT 1140
QY 1141 TCAGCCGCGGAGATTTTACGCTTACTCAGATAAATCATTTGAAGTAATAGTAA 1200
DB 1141 TCAGCCGCGGAGATTTTACGCTTACTCAGATAAATCATTTGAAGTAATAGTAA 1200
QY 1201 AACCTAGTCTTACCTTCCAGGCGCCAGGCTCAAGTAATTTGAATTCCTTACAGT 1260
DB 1201 AACCTAGTCTTACCTTCCAGGCGCCAGGCTCAAGTAATTTGAATTCCTTACAGT 1260
QY 1261 GTAGAGTAACACATTAATTTGATGATGAGAAACATGAGAAACAGTATTACAGTCT 1320
DB 1261 GTAGAGTAACACATTAATTTGATGATGAGAAACATGAGAAACAGTATTACAGTCT 1320
QY 1321 ACCAGTCTAATCAAGAAAGAAATTAACAGACTGATTTCTACAGTATGATTAATCTAA 1380
DB 1321 ACCAGTCTAATCAAGAAAGAAATTAACAGACTGATTTCTACAGTATGATTAATCTAA 1380
QY 1381 AATGAGTATCATTAAGGCTTTTGAATTTAATAAATTTGGTACTTATTAATTAATG 1440
DB 1381 AATGAGTATCATTAAGGCTTTTGAATTTAATAAATTTGGTACTTATTAATTAATG 1440
QY 1441 TAGTATTTCTGCTCCAGTTTCTTGATTAATTTGTTGATTAATTAAGATTCTGACTAT 1500
DB 1441 TAGTATTTCTGCTCCAGTTTCTTGATTAATTTGTTGATTAATTAAGATTCTGACTAT 1500
QY 1501 ATTTTAAAGGTTTCTAGTAAAGAAAGAAATGATATATCTTGAAGACATGATATACAT 1560
DB 1501 ATTTTAAAGGTTTCTAGTAAAGAAAGAAATGATATATCTTGAAGACATGATATACAT 1560
QY 1561 TATTTACACTCTTGATTTCTCAATGTAGAAATGAGAAATGCCACAAATTTGATG 1620
DB 1561 TATTTACACTCTTGATTTCTCAATGTAGAAATGAGAAATGCCACAAATTTGATG 1620
QY 1621 TAAAGTCAAGTAAACAGAGTATGTTGATCCAGGCTTTTGTCTGTTGTTTCATG 1680
DB 1621 TAAAGTCAAGTAAACAGAGTATGTTGATCCAGGCTTTTGTCTGTTGTTTCATG 1680
QY 1681 ATTCCTCTAAGCACATTCCTCAAACTTTTACACAGTATTCACACTTTGTAATTTG 1740
DB 1681 ATTCCTCTAAGCACATTCCTCAAACTTTTACACAGTATTCACACTTTGTAATTTG 1740
QY 1741 GAAAGTTTACCTGTATGTAATCAAGATGCTTCAACTGMAAAACATATCCAAATA 1800
DB 1741 GAAAGTTTACCTGTATGTAATCAAGATGCTTCAACTGMAAAACATATCCAAATA 1800
QY 1801 ATGAGGAATGTGTGCTCAGTACAGTACAGTCCAGAGGACAGTCAATTTAGGTTGC 1860
DB 1801 ATGAGGAATGTGTGCTCAGTACAGTACAGTCCAGAGGACAGTCAATTTAGGTTGC 1860
QY 1861 CTGTATTCACAGTACCTGCGGCGCTGTTTCCCGTGGGCTCTGCGGCTGCTTCCCT 1920
DB 1861 CTGTATTCACAGTACCTGCGGCGCTGTTTCCCGTGGGCTCTGCGGCTGCTTCCCT 1920
QY 1921 CTCATGCTGTTTGAATTTCTCTCAGGCTGCTAGCAAGTTCTGATCTTATACCAACA 1980
DB 1921 CTCATGCTGTTTGAATTTCTCTCAGGCTGCTAGCAAGTTCTGATCTTATACCAACA 1980
QY 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
DB 1981 CAGCAACATCCAGAAATTAAGTTCT 2005

```

```

RESULT 3
AAD38604
ID AAD38604 standard; cDNA; 2069 BP.
AC
XX AAD38604;
XX
DT 23-SEP-2002 (first entry)

```

```

XX XX
DE Human alpha-methylacyl-CoA racemase SV1 cDNA #2.
XX
KW Human: prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
KW cytosolic; SV1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 90..1238
FT /tag="a
FT /product="Human SV1 protein #2"
XX
PN WO200227324-A2.
XX
PD 04-APR-2002.
XX
PE 28-SEP-2001; 2001WO-US30532.
XX
PR 28-SEP-2000; 2000US-236238P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Richardson J, Monahan J;
XX
DR WPI: 2002-405070/43;
XX P-PSDB: AAE23972.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients.
PT Compiles measuring expression or activity of alpha-methylacyl-CoA
PT racemase
XX
PS Claim 54; Fig 3; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether
CC an individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of
CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
CC in diagnostic methods, drug screening assays, and in treating or
CC preventing cancer. e.g. prostate cancer. The present sequence is human
CC alpha-methyl-acyl-CoA racemase SV1 cDNA.
XX
SQ Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 other;
XX
Query Match 99.9%; Score 2003.4; DB 24; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTGCAAGCTGCTGGGCTGAGGCTTAAGGCTGCTCAAGTTCTTCCACGCGGCACTGGAA 60
DB 1 TTGCAAGCTGCTGGGCTGAGGCTTAAGGCTGCTCAAGTTCTTCCACGCGGCACTGGAA 84
QY 61 GCGCATGACACAGCAGAGGATCTGCTGCTGAGAGTCTCCGCGCGGCGCGGCGCT 120
DB 61 GCGCATGACACAGCAGAGGATCTGCTGCTGAGAGTCTCCGCGCGGCGCGGCGCT 144
QY 121 TCTGTCTATGCTCAGTCTGAGCTTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 TCTGTCTATGCTCAGTCTGAGCTTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
QY 145 TCTGTCTATGCTCAGTCTGAGCTTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 145 TCTGTCTATGCTCAGTCTGAGCTTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 264
QY 181 CCGGCTAAGCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 CCGGCTAAGCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 264
QY 241 AGCGGCGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 AGCGGCGGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
QY 301 CTTTCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 CTTTCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384

```

QY 361 ATCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTTCGCCGT 420
 DB 385 ATCCAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTTCGCCGT 444
 QY 421 TAGCTGGCCAGATATCAATATTTGCTTTCAGAGTGTTCCTCAAAAATTTGGCAGAA 480
 DB 445 TAGCTGGCCAGATATCAATATTTGCTTTCAGAGTGTTCCTCAAAAATTTGGCAGAA 504
 QY 481 GTGGAGAAATCCGTAATGCCCGCTGAATCTCGTGGCTGACTTTGGTGGTGGTGGT 540
 DB 505 GTGGAGAAATCCGTAATGCCCGCTGAATCTCGTGGCTGACTTTGGTGGTGGTGGT 564
 QY 541 TGTGTGCACTGGGATTTAATAGCTTTTTCACCGGACAGCCAGCCAGGAGTTCAG 600
 DB 565 TGTGTGCACTGGGATTTAATAGCTTTTTCACCGGACAGCCAGCCAGGAGTTCAG 624
 QY 601 TCAATGATGCAATATGTGTGGAGAAACAGCATATTTAAGTTCTTTCTGTGAAAATC 660
 DB 625 TCAATGATGCAATATGTGTGGAGAAACAGCATATTTAAGTTCTTTCTGTGAAAATC 684
 QY 661 AGAATCGAGTGTGGAGAACCTTCAGAGCAGAACTGTGGATGTGGACACCTT 720
 DB 685 AGAATCGAGTGTGGAGAACCTTCAGAGCAGAACTGTGGATGTGGACACCTT 744
 QY 721 TCTATACGACTTACAGCAGCAGATGGGAAATTCATGGCTTTGGACATAGAACCC 780
 DB 745 TCTATACGACTTACAGCAGCAGATGGGAAATTCATGGCTTTGGACATAGAACCC 804
 QY 781 AGTTCTAGAGCTGTGATCAAAAGCACTTGAAGCTGATGAATCTTCCCAATGAG 840
 DB 805 AGTTCTAGAGCTGTGATCAAAAGCACTTGAAGCTGATGAATCTTCCCAATGAG 864
 QY 841 TGGACATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATCTATTGCCAAAGAA 900
 DB 865 TGGACATGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATCTATTGCCAAAGAA 924
 QY 901 CGAAGCGAGAGTGTGTCAATCTTTGACGGCACAGATGCTGTGTGACTCGGTTCTGA 960
 DB 925 CGAAGCGAGAGTGTGTCAATCTTTGACGGCACAGATGCTGTGTGACTCGGTTCTGA 984
 QY 961 CTTTGTAGAGGTTTTCATCATGATCACAACAAAGGAGGCTCGTTTATCCAGTG 1020
 DB 985 CTTTGTAGAGGTTTTCATCATGATCACAACAAAGGAGGCTCGTTTATCCAGTG 1044
 QY 1021 AGGAGCAGAGCTGAGCCCGCCCTGCACTCTGCTGTTAAACCCCAAGCATCCCTT 1080
 DB 1045 AGGAGCAGAGCTGAGCCCGCCCTGCACTCTGCTGTTAAACCCCAAGCATCCCTT 1104
 QY 1081 CTTTCAAAAGGATCTTTCATAGAGAACACACTGAGAGATCTTGAATAAATTTGGAT 1140
 DB 1105 CTTTCAAAAGGATCTTTCATAGAGAACACACTGAGAGATCTTGAATAAATTTGGAT 1164
 QY 1141 TCAGCCGGGAGAGATTTATCAGCTTACAGATTAATTCATTTGAAGTAATTAAGTAA 1200
 DB 1165 TCAGCCGGGAGAGATTTATCAGCTTACAGATTAATTCATTTGAAGTAATTAAGTAA 1224
 QY 1201 AAGCTAGTCTTACCTTCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCAATTTACAT 1260
 DB 1225 AAGCTAGTCTTACCTTCAGGCCCAAGGCTCAAGTGAATTTGAATCTGCAATTTACAT 1284
 QY 1261 GTAGAGTAACATTAACATTTGATGATGAGAAACATGAGAAACAGTATTCACATGTCT 1320
 DB 1285 GTAGAGTAACATTAACATTTGATGATGAGAAACATGAGAAACAGTATTCACATGTCT 1344
 QY 1321 ACCACTCTAATCAGAAAGAAATTTACAGACTGATTTACAGTATGATTTGAATTTCTAA 1380
 DB 1345 ACCACTCTAATCAGAAAGAAATTTACAGACTGATTTACAGTATGATTTGAATTTCTAA 1404
 QY 1381 AATGATTTATCCTTATGGCTTTGATTTATTAACCTTTGGTACTTATACATAATTTATG 1440
 DB 1405 AATGATTTATCCTTATGGCTTTGATTTATTAACCTTTGGTACTTATACATAATTTATG 1464

QY 1441 TAGTTATTTCTCCCTCCAGTTTCTTGATATATTTGTTGATTTAAGATTTCTTACTAT 1500
 DB 1465 TAGTTATTTCTCCCTCCAGTTTCTTGATATATTTGTTGATTTAAGATTTCTTACTAT 1524
 QY 1501 ATTTGATGAGGTTCTAGTGAAGAAAGATATATTTCTTGAAGACATGATATACAT 1560
 DB 1525 ATTTGATGAGGTTCTAGTGAAGAAAGATATATTTCTTGAAGACATGATATACAT 1584
 QY 1561 TATTTACACTTGTATTTCAATATGAGAAATGAGAAATGAGAAATGAGAAATTTGATG 1620
 DB 1585 TATTTACACTTGTATTTCAATATGAGAAATGAGAAATGAGAAATGAGAAATTTGATG 1644
 QY 1621 TAAAGTACAGTGAAGAAAGATATTTGATGTTGATGTTGATGTTGATGTTGATG 1680
 DB 1645 TAAAGTACAGTGAAGAAAGATATTTGATGTTGATGTTGATGTTGATGTTGATG 1704
 QY 1681 ATCTCCCTTAAGCAATTCGAAAGTTTACAGAGTATTCACACTTTGTAATTTGCA 1740
 DB 1705 ATCTCCCTTAAGCAATTCGAAAGTTTACAGAGTATTCACACTTTGTAATTTGCA 1764
 QY 1741 GAAAGTTTCACTGTATTTGAATCAGAAATGCTTCAACTGAAAAAATATCCAAATA 1800
 DB 1765 GAAAGTTTCACTGTATTTGAATCAGAAATGCTTCAACTGAAAAAATATCCAAATA 1824
 QY 1801 ATGAGAAATGTGTTGCTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1860
 DB 1825 ATGAGAAATGTGTTGCTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1884
 QY 1861 CTGTATCCAGTACCTGAGGCTGTTTCCCGTGGGCTCTGGGCTGTCAAGCTTTCCTT 1920
 DB 1885 CTGTATCCAGTACCTGAGGCTGTTTCCCGTGGGCTCTGGGCTGTCAAGCTTTCCTT 1944
 QY 1921 CTCATGCTTTGATTTCTCTCAGGCTGTAGCAAGTTTGTGATTTATACCAACACA 1980
 DB 1945 CTCATGCTTTGATTTCTCTCAGGCTGTAGCAAGTTTGTGATTTATACCAACACA 2004
 QY 1981 CAGCAATCCAGAAATTAAGTTCT 2005
 DB 2005 CAGCAATCCAGAAATTAAGTTCT 2029
 RESULT 4
 ABV21293
 ID ABV21293 standard; cDNA; 2376 BP.
 XX
 AC ABV21293;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21284.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-0505171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-199862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLSNINUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX

Oy	1741	GAAGATTTCCACCGTGTATGAACTACAGAAATGCCCTTCACTGAAAAAACAATATCCAAAAATA	1800
Db	1776	GAAGATTTCCACCGTGTATGAACTACAGAAATGCCCTTCACTGAAAAAACAATATCCAAAAATA	1835
Oy	1801	ATAGAGAAATGTGTGGGTCTACTACGTAAAGTCCAGAGGACAGTCAAGTTTATAGGGTTGC	1860
Db	1836	ATAGAGAAATGTGTGGGTCTACTACGTAAAGTCCAGAGGACAGTCAAGTTTATAGGGTTGC	1895
Oy	1861	CTGTATTCACGTAACTCGGGGCGCTGTTCCTCCCGGAGGTCTGTGGGCTGTACGTTTCCTTT	1920
Db	1896	CTGTATTCACGTAACTCGGGGCGCTGTTCCTCCCGGAGGTCTGTGGGCTGTACGTTTCCTTT	1955
Oy	1921	CTCCATGTGTGTGATTTCTCTCCAGGCTGGTAGCAAGTTCTTGATATCCCAACACA	1980
Db	1956	CTCCATGTGTGTGATTTCTCTCCAGGCTGGTAGCAAGTTCTTGATATCCCAACACA	2015
Oy	1981	CAGCAACATCCAGAAATTAAGTTCT	2005
Db	2016	CAGCAACATCCAGAAATTAAGTTCT	2040
RESULT 5			
ID	ABV21881	standard; cDNA; 2376 bp.	
XX	AC	ABV21881:	
XX	AT	13-SEP-2002 (first entry)	
XX	DE	Human prostate expression marker cDNA 21872.	
XX	HM	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;	
XX	XX	pharmacogenomic marker; gene; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200160860-A2.	
XX	PD	23-AUG-2001.	
XX	PE	20-FEB-2001; 2001WO-US05171.	
XX	PR	16-FEB-2000; 2000US-183319P.	
XX	PR	16-MAR-2000; 2000US-189862P.	
XX	PR	25-MAY-2000; 2000US-207454P.	
XX	PR	09-JUN-2000; 2000US-211314P.	
XX	PR	18-JUL-2000; 2000US-219007P.	
XX	PR	13-DEC-2000; 2000US-255281P.	
XX	PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX	PI	Schlegel R, Endege WO, Monahan JE;	
XX	DR	WPI; 2001-662795/76.	
PT	XX	Novel isolated nucleic acid molecule associated with cancerous state of	
PT	XX	prostate cells and correlating with presence of prostate cancer, useful	
PT	XX	for detecting presence of prostate cancer, stage of prostate cancer -	
PS	XX	Claim 1; Page 3719; 11750pp; English.	
CC	XX	The invention relates to an isolated nucleic acid molecule (i) comprising	
CC	XX	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the	
CC	XX	specification or its complement; (i) is useful for:	
CC	XX	(a) assessing whether a patient is afflicted with prostate cancer;	
CC	XX	(b) monitoring the progression of prostate cancer in a patient;	
CC	XX	(c) assessing the efficacy of a test compound to inhibit prostate	
CC	XX	cancer in a patient;	
CC	XX	(d) assessing the efficacy of a therapy for inhibiting prostate cancer	
CC	XX	in a patient;	
CC	XX	(e) selecting a composition for inhibiting prostate cancer in a patient;	
CC	XX	(f) assessing the prostate cell carcinogenic potential of a compound;	
CC	XX	(g) determining whether prostate cancer has metastasized in a patient;	

CC	(h) assessing the aggressiveness or indolence of prostate cancer in a
CC	patient.
CC	(i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX	
S0	Sequence 2376 BP: 621 A; 512 C; 609 G; 634 T; 0 other;
	Query Match 99.7%; Score 1998.6; DB 23; Length 2376;
	Best Local Similarity 99.8%; Pred. No. 0;
	Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps
OY	1 TTGACAGCGCTGTGGCGTGGGGCTTAAGGGCTGCACTTTCCTTCAGCGGGGACATGGGAA 60
Db	36 TTGACAGCGCTGTGGCGTGGGGCTTAAGGGCTGCTCACTTTCCTTCAGCGGGGACATGGGAA 95
OY	61 GGGCCATGGCACTCAGAGGCATCTCGGCTGGAGGCTGTCGGCCCTGGCCCGGCCCT 120
Db	96 GGGCCATGGCACTCAGAGGCATCTCGGCTGGAGGCTGTCGGCCCTGGCCCGGCCCT 159
OY	121 TCTGTGCTATGTCGTGGGTGACCTTCGGGGGGGTGTGGTACGGGTGGACCGGGCGCT 180
Db	156 TCTGTGCTATGTCGTGGGTGACCTTCGGGGGGGTGTGGTACGGGTGGACCGGGCGCT 215
OY	181 CCGCGTACGACGTGACCGCTTGGCGGGGGGACAGCGGTGCTGTGCTGAGACCTGAAAC 240
Db	216 CCGCGTACGACGTGACCGCTTGGCGGGGGGACAGCGCTGCTGTGCTGAGACCTGAAAC 275
OY	241 AGCCGCGGGGAGCCCGCTGCTGGCGCGCTGTGTGCAAGCGGTCCGATGTGCTGTGAGC 300
Db	276 AGCCGCGGGGAGCCCGCTGCTGGCGCGCTGTGTGCAAGGGGTCCGATGTGCTGTGAGC 335
OY	301 CCTTCCGCGCGGTGTGTCATGAGAAATCCACAGTGGGGCCAGAGATTTCTGACAGGGAAA 360
Db	336 CCTTCCGCGCGGTGTGTCATGAGAAATCCACAGTGGGGCCAGAGATTTCTGACAGGGAAA 395
OY	361 ATCCAGAGCTTATTTATGCGACAGCTGAGTGGATTTTGGCACTAGAAAGCTTCTCCGGT 420
Db	396 ATCCAGAGCTTATTTATGCGACAGCTGAGTGGATTTTGGCACTAGAAAGCTTCTCCGGT 455
OY	421 TTAGCGGCGACGATATCAACTATTTTGGCTTTGACAGTGTCTCTCAAAAATTTGACAGAA 480
Db	456 TTAGCGGCGACGATATCAACTATTTTGGCTTTGACAGTGTCTCTCAAAAATTTGACAGAA 515
OY	481 GTGGTGAAATACCGTATGCGCCCGCTGATCTCCTGGCTGACTTTTGTGCTGGTGTGCTCTTA 540
Db	516 GTGGTGAAATACCGTATGCGCCCGCTGATCTCCTGGCTGACTTTTGTGCTGGTGTGCTCTTA 575
OY	541 TGTGTGCACTGGGATTATTAATGAGCTCTTTTACCGCACAGCACTGGCAAGGGTCAGG 600
Db	576 TGTGTGCACTGGGATTATTAATGAGCTCTTTTACCGCACAGCACTGGCAAGGGTCAGG 635
OY	601 TCATTGATGCAAAATATGTGTGGAAGGACAGCATTTTAAAGTTCTTTCTGTGGAATAATC 660
Db	636 TCATTGATGCAAAATATGTGTGGAAGGACAGCATTTTAAAGTTCTTTCTGTGGAATAATC 699
OY	661 AGAAATGAGTGTGTGGGAAGACCTGAGACAGAAACAATGTGGATGGTGGAGCAACCTT 720
Db	696 AGAAATGAGTGTGTGGGAAGACCTGAGACAGAAACAATGTGGATGGTGGAGCAACCTT 755
OY	721 TCTATACACTTACAGACAGCAAGATGGGAAATTCATGCTGTGTTGAGACATTAAGACCC 780
Db	756 TCTATACACTTACAGACAGCAAGATGGGAAATTCATGCTGTGTTGAGACATTAAGACCC 815
OY	781 AGTTCTACGAGCTGTGATCAAGGACCTTGAGCTAAAGTCTGTATGAACCTTCCCATCAGA 840
Db	816 AGTTCTACGAGCTGTGATCAAGGACCTTGAGCTAAAGTCTGTATGAACCTTCCCATCAGA 875
OY	841 TTAGCATGGAATGTGGCCAGAAATGAAGAAGATTTTCCAGATGTATTTTGGCAAGAAGA 900
Db	876 TTAGCATGGAATGTGGCCAGAAATGAAGAAGATTTTCCAGATGTATTTTGGCAAGAAGA 935
OY	901 CGAAGGCAAGATGTGTCAAAATCTTTGACGGCACAGATGCTGTGTACTCCGGTTCGA 960
Db	936 CGAAGGCAAGATGTGTCAAAATCTTTGACGGCACAGATGCTGTGTACTCCGGTTCGA 995

```

OY 961 CTTTGGAGAGGTTGTTTCATCATGATCACAAAGAGAACGGGCTGTTTATCACCAGTG 1020
    |||||||
DB 996 CTTTGGAGAGGTTGTTTCATCATGATCACAAAGAGAGGGGCTGTTTATCACCAGTG 1055
OY 1021 AGGAGACAGACGTGAGCCCCCGCCCTGACCTCTGCTGTTTAAACCCCGACCATCCCTT 1080
    |||||||
DB 1056 AGGAGACAGACGTGAGCCCCCGCCCTGACCTCTGCTGTTTAAACCCCGACCATCCCTT 1115
OY 1081 CTTTCAAAAGGAGTCCCTTTCATAGGAGAACCACTGAGGAGTACTTGAAGAAATTTGAT 1140
    |||||||
DB 1116 CTTTCAAAAGGAGTCCCTTTCATAGGAGAACCACTGAGGAGTACTTGAAGAAATTTGAT 1175
OY 1141 TCAGCCGCGAAGAGATTATCAGCTTAACCTCAGATTAATAATCATTTGAAGTAATAGTAA 1200
    |||||||
DB 1176 TCAGCCGCGAAGAGATTATCAGCTTAACCTCAGATTAATAATCATTTGAAGTAATAGTAA 1235
OY 1201 AAGCTAGTCTTAACCTTCCAGGCCCCACGGCTCAAGTAATTTGAATTTGATTTACAGT 1260
    |||||||
DB 1236 AAGCTAGTCTTAACCTTCCAGGCCCCACGGCTCAAGTAATTTGAATTTGATTTACAGT 1295
OY 1261 GTAGAGTAACACATTAACATTTGATGATGGAACATGAGAACAGTATTACAGTCTCT 1320
    |||||||
DB 1296 GTAGAGTAACACATTAACATTTGATGATGGAACATGAGAACAGTATTACAGTCTCT 1355
OY 1321 ACCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCAAGCTGATGATTTGAATCTAA 1380
    |||||||
DB 1356 ACCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCAAGCTGATGATTTGAATCTAA 1415
OY 1381 AATGCTTATTCATTTAGGGCTTTGATTTATTAATAAATTTGGTACTATTAATAATATG 1440
    |||||||
DB 1416 AATGCTTATTCATTTAGGGCTTTGATTTATTAATAAATTTGGTACTATTAATAATATG 1475
OY 1441 TACTTATTCCTCCCTCAGTTCTGATATTTGTTGATTTAAGATTTCTGACTTAT 1500
    |||||||
DB 1476 TACTTATTCCTCCCTCAGTTCTGATATTTGTTGATTTAAGATTTCTGACTTAT 1535
OY 1501 ATTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATCTTTGAAGACATGATATACAT 1560
    |||||||
DB 1536 ATTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATCTTTGAAGACATGATATACAT 1595
OY 1561 TATTTACACCTGATTTCTATCAATGTAGAAATGAGAAATGGCACAAATTTGATGTGA 1620
    |||||||
DB 1596 TATTTACACCTGATTTCTATCAATGTAGAAATGAGAAATGGCACAAATTTGATGTGA 1655
OY 1621 TAAAGTCACTGAGTAAACAGAGTATGTTGATCCAGGCTTTGCTTGCTGATGATG 1680
    |||||||
DB 1656 TAAAGTCACTGAGTAAACAGAGTATGTTGATCCAGGCTTTGCTTGCTGATGATG 1715
OY 1681 ATCTCCCTCTAAGCACATTTCCAAACTTTTACCAACAGTTATCAGACTTTGTAATTTGCAA 1740
    |||||||
DB 1716 ATCTCCCTCTAAGCACATTTCCAAACTTTTACCAACAGTTATCAGACTTTGTAATTTGCAA 1775
OY 1741 GAAAGTTTCACTGATTAATGAATCAGAAATGCCCTTCAACCTGAAAAAACAATATCCAAATA 1800
    |||||||
DB 1776 GAAAGTTTCACTGATTAATGAATCAGAAATGCCCTTCAACCTGAAAAAACAATATCCAAATA 1835
OY 1801 ATGAGAAATGTGTGGCTCACTAGCTAGAGTCCAGAGGAGACAGTCAAGTTTAGGGTGC 1860
    |||||||
DB 1836 ATGAGAAATGTGTGGCTCACTAGCTAGAGTCCAGAGGAGACAGTCAAGTTTAGGGTGC 1895
OY 1861 CTGTATTCACAGTAACTGAGGCGCTGTTTCCCGTGGGTCTCTGCGGCTGTCAGCTTCCCTT 1920
    |||||||
DB 1896 CTGTATTCACAGTAACTGAGGCGCTGTTTCCCGTGGGTCTCTGCGGCTGTCAGCTTCCCTT 1955
OY 1921 CTCAGATGTGTTTATTTCTCTCAGGCTGATACCAAGTTTGTGATCTTATACCAACACA 1980
    |||||||
DB 1956 CTCAGATGTGTTTATTTCTCTCAGGCTGATACCAAGTTTGTGATCTTATACCAACACA 2015
OY 1981 CAGCAATCAGCAAGTAAGTTCT 2005
    |||||||
DB 2016 CAGCAATCAGCAAGTAAGATCT 2040

```

```

RESULT 6
ABV25239
ID ABV25239 standard; cDNA; 2376 BP.
XX
AC ABV25239;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 25230.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4947-4948; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (i) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (ii) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other:
Query Match 99.7%; Score 1998.6; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 TTTGAGGCTGCTGGGCTGAGGCTAAGGCTGCTCAGTTTCTTCCAGCGGGCACTGGGAA 60
    |||||||
DB 36 TTTCAGGCTGCTGGGCTGAGGCTAAGGCTGCTCAGTTTCTTCCAGCGGGCACTGGGAA 95
OY 61 GCGCCATGCGACATGCAAGGCGATCTCGTGTGAGAGCTGTCCGGGCTGCGCCCGGCGCT 120
    |||||||
DB 96 GCGCCATGCGACATGCAAGGCGATCTCGTGTGAGAGCTGTCCGGGCTGCGCCCGGCGCT 155
OY 121 TCTGTCTATGCTGCTGGGCTGACTTGGGGCGGCTGTGTGATGACCGGTGACCGGCGCGCT 180
    |||||||

```


PF 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 CC 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE.
 PI WPI; 2001-662795/76.
 DR
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 5494-5495; 11750bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 XX Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;
 SQ
 Query Match 99.7%; Score 1998.6; DB 23; Length 2376;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 456 TAGTGGCCACGATATCACTATTGGCTTGTGACGCTGTTCTCTCAAAAATTGGCAGAA 515
 QY 481 GTGGTGAAGATCCGTATGCCCGCGGTGATCTCTGCTGACTTGTGCTGTGGCTTGA 540
 DB 516 GTGGTGAAGATCCGTATGCCCGCGGTGATCTCTGCTGACTTGTGCTGTGGCTTGA 575
 QY 541 TGTGTGCACTGGGCAATTATATGCTCTTTTGTGACCGCACACGACTGGCAAGGCTCAG 600
 DB 576 TGTGTGCACTGGGCAATTATATGCTCTTTTGTGACCGCACACGACTGGCAAGGCTCAG 635
 QY 601 TCATTGATGCAAAATATGTGGGAAGACAGCATATTAATGTTCTTTCTGTGAAAACCTC 660
 DB 636 TCATTGATGCAAAATATGTGGGAAGACAGCATATTAATGTTCTTTCTGTGAAAACCTC 695
 QY 661 AGAATGAGTCTGTGGGAAGACACCTGAGAGACAGAAATGTTGGATGTGGAGACCTT 720
 DB 696 AGAATGAGTCTGTGGGAAGACACCTGAGAGACAGAAATGTTGGATGTGGAGACCTT 755
 QY 721 TCTATACGACTTACAGACACAGATGGGAAATTCATGCTGTTGGAGCAATAGAACCC 780
 DB 756 TCTATACGACTTACAGACACAGATGGGAAATTCATGCTGTTGGAGCAATAGAACCC 815
 QY 781 AGTCTGACAGCTGCTGATCAAAAGACTGTGACTTAAAGTCTGATGAACTTCCCAATCAGA 840
 DB 816 AGTCTGACAGCTGCTGATCAAAAGACTGTGACTTAAAGTCTGATGAACTTCCCAATCAGA 875
 QY 841 TGACATGATGATGTGGCCAGAAATGAAGAAGAAATGTTGAGATGATTTTGCAGAAAGAGA 900
 DB 876 TGACATGATGATGTGGCCAGAAATGAAGAAGAAATGTTGAGATGATTTTGCAGAAAGAGA 935
 QY 901 CGAAGCAGAGTGTGTCMAATCTTTGACGGCACAGATGCTGTGTACTCCGTTCTGA 960
 DB 936 CGAAGCAGAGTGTGTCMAATCTTTGACGGCACAGATGCTGTGTACTCCGTTCTGA 995
 QY 961 CTTTGAAGAGGTGTTCATCATCATGATFCAACAACAAGAAAGGCGCTGTTATACACAGTG 1020
 DB 996 CTTTGAAGAGGTGTTCATCATCATGATFCAACAACAAGAAAGGCGCTGTTATACACAGTG 1055
 QY 1021 AGAGCAGAGAGTGTGAGCCCGCCCGCTGACCTGCTGTGTTAAACCCCAAGCCATCCCTT 1080
 DB 1056 AGAGCAGAGAGTGTGAGCCCGCCCGCTGACCTGCTGTGTTAAACCCCAAGCCATCCCTT 1115
 QY 1081 CTTTCAAAAAGGATCCTTTTCATAGAGAACACACTGTGAGAGATCTTGAAGATTTGGAT 1140
 DB 1116 CTTTCAAAAAGGATCCTTTTCATAGAGAACACACTGTGAGAGATCTTGAAGATTTGGAT 1175
 QY 1141 TCAGCCGCGAAGATTTATCAGCTTAACCTAAGTAAATCATTAAGAAAGTAAATGAAGTAA 1200
 DB 1176 TCAGCCGCGAAGATTTATCAGCTTAACCTAAGTAAATCATTAAGAAAGTAAATGAAGTAA 1235
 QY 1201 AAGCTAGTCTCTAATCTCCAGGCCACAGGCTCAAGTGAATTTGAATCTGCATTTACAGT 1260
 DB 1236 AAGCTAGTCTCTAATCTCCAGGCCACAGGCTCAAGTGAATTTGAATCTGCATTTACAGT 1295
 QY 1261 GTAGAGTAACACATTAATGTATGATGATGGAACATGAGAGAACATTAACAGTCTCCT 1320
 DB 1296 GTAGAGTAACACATTAATGTATGATGATGGAACATGAGAGAACATTAACAGTCTCCT 1355
 QY 1321 ACCACTCAATCAAGAAAGAAATTAACAGACTCTGATCTCAAGTGAATTTGAATTTAA 1380
 DB 1356 ACCACTCAATCAAGAAAGAAATTAACAGACTCTGATCTCAAGTGAATTTGAATTTAA 1415
 QY 1381 AATGTTATCATTAAGGCTTGTGATTTATTAATTAATTTGGGTACTTTACTAATTAATG 1440
 DB 1416 AATGTTATCATTAAGGCTTGTGATTTATTAATTAATTTGGGTACTTTACTAATTAATG 1475
 QY 1441 TAGTTATTTGCTCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTGACTTAT 1500
 DB 1476 TAGTTATTTGCTCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTGACTTAT 1535
 QY 1501 ATTTGTAATGGTCTAGTGAAGAAAGAAATGATTAATTTCTTGAAGACATGATATACAT 1560
 DB 1536 ATTTGTAATGGTCTAGTGAAGAAAGAAATGATTAATTTCTTGAAGACATGATATACAT 1595

Db 622 GGTGATGATGCAAAATATGTTGGAGAACAGCATATTTAAAGTCTTTCTGTGGAAAC 681
 QY TCAGAAATGAGTCTGTGGAGAACCTCGAGAGCAAGACATGTGGATGGAGACACC 718
 Db 682 TCAGAAATGAGTCTGTGGAGAACCTCGAGAGCAAGACATGTGGATGGAGACACC 741
 QY TTTCTATGAGCTTTACAGAGCAGACAGATGGGAAATTCATGGCTTTGGAGCAATAGAAC 778
 Db 742 TTTCTATGAGCTTTACAGAGCAGACAGATGGGAAATTCATGGCTTTGGAGCAATAGAAC 801
 QY CCAGTCTACAGCTCTGTATCAAAAGACTTGGACTAAAGTCTGATGAAGTCTCCCATCA 838
 Db 802 CCAGTCTACAGCTCTGTATCAAAAGACTTGGACTAAAGTCTGATGAAGTCTCCCATCA 861
 QY GATGACATGATGATTTGGCCAGAAATGAAGAAGTGTGAGATGTATTTCCAAAGAA 898
 Db 862 GATGACATGATGATTTGGCCAGAAATGAAGAAGTGTGAGATGTATTTCCAAAGAA 921
 QY GACGAAGCAGAGTGTGTCAAATCTTTGACGGCAGACAGATGCTGTGATCCGGTCT 958
 Db 922 GACGAAGCAGAGTGTGTCAAATCTTTGACGGCAGACAGATGCTGTGATCCGGTCT 981
 QY GACTTTGAGAGGCTTTCATCATATCAACAAGGAGGAGGCTGCTTTATCAACCA 1018
 Db 982 GACTTTGAGAGGCTTTCATCATATCAACAAGGAGGAGGCTGCTTTATCAACCA 1041
 QY TGAGAGCAGAGAGTGTGAGCCCGCCCTGCTGCTTTAAACCCAGCCATCCC 1078
 Db 1042 TGAGAGCAGAGAGTGTGAGCCCGCCCTGCTGCTTTAAACCCAGCCATCCC 1101
 QY TTTCTTCAAAAGGAGTCTTTCTATGAGAGACACACTGAGAGATCTTGAAAGTGTG 1138
 Db 1102 TTTCTTCAAAAGGAGTCTTTCTATGAGAGACACACTGAGAGATCTTGAAAGTGTG 1161
 QY ATTACAGCCGAGAGATTTATGATTAAGTAAATGATGAAGTAAATGATTAAGT 1198
 Db 1162 ATTACAGCCGAGAGATTTATGATTAAGTAAATGATGAAGTAAATGATTAAGT 1221
 QY AAAAGTAGTCTTAATCTTCAAGCCAGGCTCAAGTGAATTTGAATCTGCAATTTACA 1258
 Db 1222 AAAAGTAGTCTTAATCTTCAAGCCAGGCTCAAGTGAATTTGAATCTGCAATTTACA 1281
 QY GTGTAAAGTAAACATTAATGATGATGAAGACATGAGAGACAGATTTACAGTGT 1318
 Db 1282 GTGTAAAGTAAACATTAATGATGATGAAGACATGAGAGACAGATTTACAGTGT 1341
 QY CTACCTCTAATCAAGAAAGAAATTACAGACTGATTTCTAGTATGATTAAGTGT 1378
 Db 1342 CTACCTCTAATCAAGAAAGAAATTACAGACTGATTTCTAGTATGATTAAGTGT 1401
 QY AAAAATGTTATCATTAAGGCTTTGATTTAAACTTTGGTACTTATTAATTAAT 1438
 Db 1402 AAAAATGTTATCATTAAGGCTTTGATTTAAACTTTGGTACTTATTAATTAAT 1461
 QY GGTAGTATTTGCTTCCAGTTGCTTGTATATTTGTTGATTAAGTGTACTT 1498
 Db 1462 GGTAGTATTTGCTTCCAGTTGCTTGTATATTTGTTGATTAAGTGTACTT 1521
 QY AATTTTGAATGGTCTCTGAGTGAAGAAAGATATATTTCTGAGACATCATATTTACA 1558
 Db 1522 AATTTTGAATGGTCTCTGAGTGAAGAAAGATATATTTCTGAGACATCATATTTACA 1581
 QY TTTATTTACACTCTGATTTCTACAAATGTAGAAATGAGAAATGCCAAATTTGTATGT 1618
 Db 1582 TTTATTTACACTCTGATTTCTACAAATGTAGAAATGAGAAATGCCAAATTTGTATGT 1641
 QY GATTAAGTCACTGATGAAGAGATGTTGTTGATTCACAGGCTTTTGTCTGTTGTTCA 1678
 Db 1642 GATTAAGTCACTGATGAAGAGATGTTGTTGATTCACAGGCTTTTGTCTGTTGTTCA 1701
 QY TGTATCTCCCTCTAAGCAGATTCCAAACTTTAGCAGAGATTTACACTTTGTAATTTGCA 1738
 Db 1702 TGTATCTCCCTCTAAGCAGATTCCAAACTTTAGCAGAGATTTACACTTTGTAATTTGCA 1761

QY 1739 AAGAAAGTTTCACCTGTATTTGATCAGATGCTTCAACTGAAAAAACAATCCAAA 1798
 Db 1762 AAGAAAGTTTCACCTGTATTTGATCAGATGCTTCAACTGAAAAAACAATCCAAA 1821
 QY 1799 TAATGAGAAATGTGTGCTCCTACCTAGTACAGTCCAGAGGACACTGATTTAGGTT 1858
 Db 1822 TAATGAGAAATGTGTGCTCCTACCTAGTACAGTCCAGAGGACACTGATTTAGGTT 1881
 QY 1859 GCGTGTATCCAGTAACTCGGGGCTGTTCCCGGTGGTCTCGGGCTGACGTTCTCT 1918
 Db 1882 GCGTGTATCCAGTAACTCGGGGCTGTTCCCGGTGGTCTCGGGCTGACGTTCTCT 1941
 QY 1919 TTTCCATGTGTTTGAATTTCTCCTCAGGCTGTAGCAGATTTCTGATTAACCAACA 1978
 Db 1942 TTTCCATGTGTTTGAATTTCTCCTCAGGCTGTAGCAGATTTCTGATTAACCAACA 2001
 QY 1979 CACAGCAACATCCAGAAATTAAGTTCT 2005
 Db 2002 CACAGCAACATCCAGAAATTAAGATCT 2028
 RESULT 9
 AAD38606
 ID AAD38606 standard; cDNA; 3023 BP.
 XX
 AC AAD38606;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human alpha-methylacyl-CoA racemase splice variant, SV3 cDNA.
 XX
 DE Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
 KW Cytostatic; SV3; gene; ss.
 KM
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 90..686
 FT /tag= a
 FT /product= "Human SV3 protein"
 XX
 PN WO200227324-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 28-SEP-2001; 2001MO-US30532.
 XX
 PR 28-SEP-2000; 2000US-236238P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Richardson J, Monahan J;
 XX
 PI
 XX
 DR MPI: 2002-405070/43.
 XX
 DR P-PSDB; AAE23974.
 XX
 PT Determining risk for prostate cancer in subject or risk for metastatic
 PT prostate cancer to liver or lymph nodes of prostate cancer patients,
 PT comprises measuring expression or activity of alpha-methylacyl-CoA
 PT racemase -
 XX
 PS Claim 54; Fig 7; 102pp; English.
 XX
 CC The present invention relates to novel methods for determining whether
 CC an individual is at risk for prostate cancer or whether a prostate cancer
 CC patient is at risk for metastatic prostate cancer to the liver or lymph
 CC nodes. The method involves measuring the expression or activity of
 CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
 CC in diagnostic methods, drug screening assays, and in treating or
 CC preventing cancer, e.g. prostate cancer. The present sequence is human
 CC alpha-methyl-acyl-CoA racemase splice variant, SV3 cDNA.
 CC
 XX

Sequence 3023 BP; 846 A; 621 C; 710 G; 846 T; 0 other:

Query Match 83.4%; Score 1671.4; DB 24; Length 3023;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1843; Conservative 0; Mismatches 1; Indels 161; Gaps 1;

```
OY 1 TTGCAGCGTGTGGGCTGAAGGCTGACATCTTCTTCAAGCGGCGACTGGAA 60
    |||||||
DB 25 TTGCAGCGTGTGGGCTGAAGGCTGACATCTTCTTCAAGCGGCGACTGGAA 84
OY 61 GCGCATGAGCTGAGGAGATCTGGTCTGGAGCTGCCGCGCGCGCGCGCGCT 120
    |||||||
DB 85 GCGCATGAGCTGAGGAGATCTGGTCTGGAGCTGCCGCGCGCGCGCGCGCT 144
OY 121 TCTGTCTGTGGTCTGGCTGACTTGGGGGCGGTGTGTAGCGGCGCGCGCT 180
    |||||||
DB 145 TCTGTCTGTGGTCTGGCTGACTTGGGGGCGGTGTGTAGCGGCGCGCGCT 204
OY 181 CCGGCTAGAGCTGAGCGGCTTGGGCGGGGCAAGCGCTGCTAGTGTGAGCTGAAG 240
    |||||||
DB 205 CCGGCTAGAGCTGAGCGGCTTGGGCGGGGCAAGCGCTGCTAGTGTGAGAGC 264
OY 241 AGCGCGGGGAGCGCGCGCTGCTGGCGCTGTGCAAGCGCTGATGCTGCTGAGAC 300
    |||||||
DB 265 AGCGCGGGGAGCGCGCGCTGCTGGCGCTGTGCAAGCGCTGATGCTGCTGAGAC 324
OY 301 CCTTCCGCGCGGCTGTCAATGAGAACTCCAGCTGGGCCAGAGATTCGACGCGGAAA 360
    |||||||
DB 325 CCTTCCGCGCGGCTGTCAATGAGAACTCCAGCTGGGCCAGAGATTCGACGCGGAAA 384
OY 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCGCGGT 420
    |||||||
DB 385 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTCGCGGT 444
OY 421 TACTGGCCAGATTCATCAATTTTGGCTTGTGAGGTGTCTCTCAAAAATTTGGCGAA 480
    |||||||
DB 445 TACTGGCCAGATTCATCAATTTTGGCTTGTGCA----- 479
OY 481 GTGTGAGAAATCCGTATGCCCCCGCTGAATCTCTGCGCTACCTTTCGTGTGTGGCTTGA 540
    |||||||
DB 480 ----- 479
OY 541 TGTGTCACTGGGCAATTAATGCTCTTTTGTGACGACGACGACGACGAGGCTCAGG 600
    |||||||
DB 480 ----- 479
OY 601 TCATGTATCAATATGTGTGAGAGAAACAGCATATTTAAGTTCTTTCTGTGAAAACTC 660
    |||||||
DB 480 -----GCTGGAAGAAACAGCATATTTAAGTTCTTTCTGTGAAAACTC 523
OY 661 AGAATCGAGTCTGTGGGAGCACCTCGAGGACAGAAATGTTGGATGTTGAGACACTT 720
    |||||||
DB 524 AGAATCGAGTCTGTGGGAGCACCTCGAGGACAGAAATGTTGGATGTTGAGACACTT 583
OY 721 TCTATACGACTTACAGGACAGACAGATGGGAATTCATGGCTGTGTGAGCAATACACCC 780
    |||||||
DB 584 TCTATACGACTTACAGGACAGACAGATGGGAATTCATGGCTGTGTGAGCAATACACCC 643
OY 781 AGTTTACAGCTGCTGTATCAAGAGCTTGAATTAAGTGTGATTAACCTCCATCAGA 840
    |||||||
DB 704 TGAGCATGTGATATTTGGCAGAAATGAAGAAAGTTTTCAGATGATTTTCAAAAGAGA 900
    |||||||
OY 901 CGAAGCAGAGTGTGTCTCAATCTTTTACGCGCAGAGATGCTGTGTGACTCGGTTCTGA 960
    |||||||
DB 764 CGAAGCAGAGTGTGTCTCAATCTTTTACGCGCAGAGATGCTGTGTGACTCGGTTCTGA 823
OY 961 CTTTATGAGAGGTTTTCATCATGATCACAACAGGAGGAGGCTGTTTATCACACAGTG 1020
    |||||||
DB 824 CTTTATGAGAGGTTTTCATCATGATCACAACAGGAGGAGGCTGTTTATCACACAGTG 883
```

```
OY 1021 AGGAGCAGACGTGAGCCCCCGCCCTGACATCTGCTGTTAAACACCCACCCATCCCTT 1080
    |||||||
DB 884 AGGAGCAGACGTGAGCCCCCGCCCTGACATCTGCTGTTAAACACCCACCCATCCCTT 943
OY 1081 CTTTCAAAAGGATCTTTTCAATAGAGAACACACTGAGAGATTAAGTGAATTTGGAT 1140
    |||||||
DB 944 CTTTCAAAAGGATCTTTTCAATAGAGAACACACTGAGAGATTAAGTGAATTTGGAT 1003
OY 1141 TCAGCCGGAAGATTTATAGCTTAACCTACATCAATTAATCTTGAAGTAAATAGSTAA 1200
    |||||||
DB 1004 TCAGCCGGAAGATTTATAGCTTAACCTACATCAATTAATCTTGAAGTAAATAGSTAA 1063
OY 1201 AAGCTATCTCTAATCTTCAGGCGCCAGCGCTCAAGTGAATTTGAATACGATTTACAGT 1260
    |||||||
DB 1064 AAGCTATCTCTAATCTTCAGGCGCCAGCGCTCAAGTGAATTTGAATACGATTTACAGT 1123
OY 1261 GTTGAATTAACATTAACATTTGATGATGGAACATGAGAGAAAGTATTACAGTCCCT 1320
    |||||||
DB 1124 GTTGAATTAACATTAACATTTGATGATGGAACATGAGAGAAAGTATTACAGTCCCT 1183
OY 1321 ACCACTTAATCAGAAAGAAATTAACAGACTGATTTCAAGTATGATGAATTTCTAA 1380
    |||||||
DB 1184 ACCACTTAATCAGAAAGAAATTAACAGACTGATTTCAAGTATGATGAATTTCTAA 1243
OY 1381 AAATGATTAATCAGGCTTTGATTTATAAACCTTGGTACTTATACATAATTAATG 1440
    |||||||
DB 1244 AAATGATTAATCAGGCTTTGATTTATAAACCTTGGTACTTATACATAATTAATG 1303
OY 1441 TACTTATCTGCTTCCAGTTTGGCTTATATTTGATATTTGAATTAATTTGACTTAT 1500
    |||||||
DB 1304 TACTTATCTGCTTCCAGTTTGGCTTATATTTGATATTTGAATTAATTTGACTTAT 1363
OY 1501 AATTTGAATGGGTCTGATGAGAAAGAAAGATATTTCTTGAACATGATATACATTT 1560
    |||||||
DB 1364 AATTTGAATGGGTCTGATGAGAAAGAAAGATATTTCTTGAACATGATATACATTT 1423
OY 1561 TATTTACACTCTTGAATTTTACATGTTAGAAATGAGAAATGCCCAATTTGTATGCTGA 1620
    |||||||
DB 1424 TATTTACACTCTTGAATTTTACATGTTAGAAATGAGAAATGCCCAATTTGTATGCTGA 1483
OY 1621 TAAAGTCAAGTGAACAGAGATGTTGGTTCATCCAGGCTTTTGTCTGTTGTTTCATG 1680
    |||||||
DB 1484 TAAAGTCAAGTGAACAGAGATGTTGGTTCATCCAGGCTTTTGTCTGTTGTTTCATG 1543
OY 1681 ATCTCCCTTAAGCATTTCCAACTTTAGCAACAGTATTCACACTTGTGAATTTGCCAAA 1740
    |||||||
DB 1544 ATCTCCCTTAAGCATTTCCAACTTTAGCAACAGTATTCACACTTGTGAATTTGCCAAA 1603
OY 1741 GAAAGTTTCACTGTATTTGAATGAGAAATGCTTCAACTGAAAGAAATATTCGCAAAAT 1800
    |||||||
DB 1604 GAAAGTTTCACTGTATTTGAATGAGAAATGCTTCAACTGAAAGAAATATTCGCAAAAT 1663
OY 1801 ATGAGAAATGTTGGTCTCACTACGTACAGTTCAGAGGACAGTCACTTTAGGCTTGC 1860
    |||||||
DB 1664 ATGAGAAATGTTGGTCTCACTACGTACAGTTCAGAGGACAGTCACTTTAGGCTTGC 1723
OY 1861 CTGTATCACTGTAAGTCTGGGCTTTTCCCGTGGGCTCTGCGGCTGCACTTCTCTTT 1920
    |||||||
DB 1724 CTGTATCACTGTAAGTCTGGGCTTTTCCCGTGGGCTCTGCGGCTGCACTTCTCTTT 1783
OY 1921 CTCATGTTTGTGATTTCTCTCAGGCTGTAGCAAGTTCTGATCTTATACCAACACA 1980
    |||||||
DB 1784 CTCATGTTTGTGATTTCTCTCAGGCTGTAGCAAGTTCTGATCTTATACCAACACA 1843
OY 1981 CAGCAATCATCCAGAAATTAAGTTCT 2005
    |||||||
DB 1844 CAGCAATCATCCAGAAATTAAGATCT 1868
    |||||||
```

RESULT 10
AAH13696
ID AAH13696 standard; cdna; 1674 BP.

QY 722 CTATACGACTTACAGACACACAGATGGGAAATTCATGCGCTTTGGACCAATPAGACCCCA 781
 DB 661 CTATACGACTTACAGACACACAGATGGGAAATTCATGCGCTTTGGACCAATPAGACCCCA 720
 QY 782 GTTCTACGAGCTGTGATCAAGAGACTTGAGCTGTAGTAACCTTCCCAATGAGT 841
 DB 721 GTTCTACGAGCTGTGATCAAGAGACTTGAGCTGTAGTAACCTTCCCAATGAGT 780
 QY 842 GAGCATGATGATGGCCAGCAAAATGAAGAAGAGTTTCAGATGATTTTCCAAAGAAGAC 901
 DB 781 GAGCATGATGATGGCCAGCAAAATGAAGAAGAGTTTCAGATGATTTTCCAAAGAAGAC 840
 QY 902 GAGGACAGAGTGTGTCAATCTTTACGCGCAGATGCTGTGTGATCCGGTTCGAC 961
 DB 841 GAGGACAGAGTGTGTCAATCTTTACGCGCAGATGCTGTGTGATCCGGTTCGAC 900
 QY 962 TTTTGAAGAGTGTGTATCATATCATACAAAGAGAGGGGCTCGTTTATCAGCAGTGA 1021
 DB 901 TTTTGAAGAGTGTGTATCATATCATACAAAGAGAGGGGCTCGTTTATCAGCAGTGA 960
 QY 1022 GGAGGAGAGCTGAGCCCGCCGCTGCTGCTGTTAAACCCGACGATCCCTTC 1081
 DB 961 GGAGGAGAGCTGAGCCCGCCGCTGCTGCTGTTAAACCCGACGATCCCTTC 1020
 QY 1082 TTTTCAAAAGGATCTCTTCAATAGAGACACATGAGAGATCTTGAAGAATTTGAT 1141
 DB 1021 TTTTCAAAAGGATCTCTTCAATAGAGACACATGAGAGATCTTGAAGAATTTGAT 1080
 QY 1142 CAGCCGCGAGAGATTTTATCAGCTTAATCACTCAATTAATTAATTAATTAATTAAT 1201
 DB 1081 CAGCCGCGAGAGATTTTATCAGCTTAATCACTCAATTAATTAATTAATTAATTAAT 1140
 QY 1202 AGCTAGTCTTCACTTCACTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
 DB 1141 AGCTAGTCTTCACTTCACTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 QY 1262 TAGAGTAAACATTAATCTGATGAGAAATGAGAAAGTATTAAGTCTGCTA 1321
 DB 1201 TAGAGTAAACATTAATCTGATGAGAAATGAGAAAGTATTAAGTCTGCTA 1260
 QY 1322 CCAGCTTAATCAAGAAAGATTAACAGACTGATTAACAGATGATTAATTAATTAATTAAT 1381
 DB 1261 CCAGCTTAATCAAGAAAGATTAACAGACTGATTAACAGATGATTAATTAATTAATTAAT 1320
 QY 1382 AATGCTTAATCAATGAGGCTTTGATTAATTAATTAATTAATTAATTAATTAATTAAT 1441
 DB 1321 AATGCTTAATCAATGAGGCTTTGATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
 QY 1442 AGTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
 DB 1381 AGTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 QY 1502 TTTTGAATGAGTCTTACTGAAAGAAAGATTAATTTCTTGAAGACATCGATTAATTAAT 1561
 DB 1441 TTTTGAATGAGTCTTACTGAAAGAAAGATTAATTTCTTGAAGACATCGATTAATTAAT 1500
 QY 1562 AATTACACTGTTGATTTACAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 1621
 DB 1501 AATTACACTGTTGATTTACAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 1560
 QY 1622 AAAAGTCACTGAGAAACAGA 1640
 DB 1561 AAAAGTCACTGAGAAACAGA 1579
 RESULT 13
 ID AAA06347 standard; cDNA; 1621 BP.
 AC AAA06347;
 XX
 XX
 XX 13-JUN-2000 (first entry)
 XX

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:107.
 XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW Immunogenic; cytostatic; vaccine; ss.
 XX
 OS Homo sapiens.
 PN WO200004149-A2.
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99MO-US15838.
 XX
 PR 14-JUL-1998; 98US-0115453.
 PR 14-JUL-1998; 98US-0116134.
 PR 23-SEP-1998; 98US-0159812.
 PR 23-SEP-1998; 98US-0159822.
 PR 15-JAN-1999; 99US-0232149.
 PR 15-JAN-1999; 99US-0232880.
 PR 09-APR-1999; 99US-0286946.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Dillon DC, Harlocker SL, Yudin J, Xu J, Mitcham JL.
 DR WPI: 2000-171268/15.
 XX
 PT New polypeptide useful for treating and diagnosing prostate cancer
 PT comprises an immunogenic portion of prostate tumor protein.
 XX
 PS Claim 1: Page 133-134; 263pp; English.
 XX
 CC The present invention describes isolated polypeptides, comprising an
 CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express
 CC the polypeptides, antibodies against the polypeptides and vaccines
 CC comprising them can be used for inhibiting the development of prostate
 CC cancer in a patient. The polypeptides can be used to generate antibodies
 CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
 CC the polynucleotides encoding the polypeptides can be used as a probe or
 CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
 CC AA82000 to AA82020 represent sequences used in the exemplification of
 CC the present invention.
 XX
 SO Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
 XX
 Query Match 78.5%; Score 1574.2; DB 21; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 62 CGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 121
 DB 1 CGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 60
 QY 122 CTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 DB 61 CTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 182 CGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 241
 DB 121 CGCATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 180
 QY 242 GCGGCGGAGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
 DB 181 GCGGCGGAGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 302 CTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
 DB 241 CTTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 362 TCCAGAGCTTATTTATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 421

```

|||||
Db 301 TCCAAAGCTTATTTATGCCAGGCTGAGTGGATTGGCCATCAGGAAGCTTCGCGGTT 360
QY 422 AGCTGGCCACGATATCACTAATTTGGCTTTTCAGGTTGTTCTCTCAAAAATTTGGCAGAG 481
Db 361 AGCTGGCCACGATATCACTAATTTGGCTTTTCAGGTTGTTCTCTCAAAAATTTGGCAGAG 420
QY 482 TGGTGAAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTCGTGGTGGCCCTTAT 541
Db 421 TGGTGAAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTCGTGGTGGCCCTTAT 480
QY 542 GTGTGACATCGGATATATATGCTCTTTTTCACCCGACACGACATCGGAGAGGTGAGT 601
Db 481 GTGTGACATCGGATATATATGCTCTTTTTCACCCGACACGACATCGGAGAGGTGAGT 540
QY 602 CATTGATGCAAAATATGTTGGTGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAACTCA 661
Db 541 CATTGATGCAAAATATGTTGGTGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAACTCA 600
QY 662 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGTGAGACACCTTT 721
Db 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGTGAGACACCTTT 660
QY 722 CTATACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGGACCAATTAACCCCA 781
Db 661 CTATACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGGACCAATTAACCCCA 720
QY 782 GTTCTACGAGCTCTGATCAAAAGACTTGGACTAAAGTGTGATGACTTCCCAATCAGAT 841
Db 721 GTTCTACGAGCTCTGATCAAAAGACTTGGACTAAAGTGTGATGACTTCCCAATCAGAT 780
QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAAAGTTGACATGATATTTGCAAAAGAAC 901
Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAAGTTGACATGATATTTGCAAAAGAAC 840
QY 902 GAAGGAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTTCTGAC 961
Db 841 GAAGGAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTTCTGAC 900
QY 962 TTTTGAAGAGTTGTCATCATGATGATCAACAAGAAAGGGGCTGTTATCAACAGTGA 1021
Db 901 TTTTGAAGAGTTGTCATCATGATGATCAACAAGAAAGGGGCTGTTATCAACAGTGA 960
QY 1022 GGAGCAGAGAGTGAGCCCGCCCTGACCTGTCTGTTAAACACCCACCATCCCTTC 1081
Db 961 GGAGCAGAGAGTGAGCCCGCCCTGACCTGTCTGTTAAACACCCACCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTGATAGAGAACACACTGAGAGATCTGTAAGAAATTTGGATT 1141
Db 1021 TTTCAAAAGGATCTTTGATAGAGAACACACTGAGAGATCTGTAAGAAATTTGGATT 1080
QY 1142 CAGCCGCGAAGAGATTTATCAGCTTAACATCAGATTAATAATCATTTAAGTAA 1201
Db 1081 CAGCCGCGAAGAGATTTATCAGCTTAACATCAGATTAATAATCATTTAAGTAA 1140
QY 1202 AGCTAATCTCTAATCTTCAGGCCCCAGGCTCAAGTGAATTTGAATCTGATTTACAGT 1261
Db 1141 AGCTAATCTCTAATCTTCAGGCCCCAGGCTCAAGTGAATTTGAATCTGATTTACAGT 1200
QY 1262 TAGAGTACACATATGATGATGAGTGAAGATGAGAGATTAAGTAACTGATGCTT 1321
Db 1201 TAGAGTACACATATGATGATGAGTGAAGATGAGAGATTAAGTAACTGATGCTT 1260
QY 1322 CCACCTAATCAAGAAAGATTTACAGACTGATTTCTACAGTATGATGATTTGATTA 1381
Db 1261 CCACCTAATCAAGAAAGATTTACAGACTGATTTCTACAGTATGATGATTTGATTA 1320
QY 1382 AATGTTATCATTAAGGCTTTTGATTTATTAATACTTTGGTACTTATTAATAATATG 1441
Db 1321 AATGTTATCATTAAGGCTTTTGATTTATTAATACTTTGGTACTTATTAATAATATG 1380
QY 1442 AGTATATTCGCTTCCAGTTTGTGATATATTTGATATTAAGATCTTTACTTATA 1501
|||||

```

```

Db 1381 AGTATATTCGCTTCCAGTTTGTCTGATATATTTGTTGATATTAACATTTCTGACTTATA 1440
QY 1502 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATATTTCTTGAAGACATGATATACATT 1561
Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAGATGATATATTTCTTGAAGACATGATATACATT 1500
QY 1562 ATTTACACTCTGATTTCTACATATGTAAGAAATGAGAAATGCCACAATTTGATGAT 1621
Db 1501 ATTTACACTCTGATTTCTACATATGTAAGAAATGAGAAATGAGAAATGATGATGAT 1560
QY 1622 AAAAGTCAGTGAACAGA 1640
Db 1561 AAAAGTCAGTGAACAAA 1579

RESULT 14
AAS63555
ID AAS63555 standard; cDNA; 1621 BP.
XX
AC AAS63555;
XX
DT 29-JAN-2002 (first entry)
DE Human prostate cDNA sequence #107.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retler MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
DR WPI: 2001-639232/73.
DR P-PsDB; AAU69761.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 264-265; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.

```


